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GenCore version 5.1.3
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OM protein - protein search, using sw model

November 21, 2002, 13:40:47; Search time 11 Seconds (without alignments) 203.611 Million cell updates/sec Run on:

US-09-776-724A-142 283 1 MRRCVRHVLGIGLIVLKNLY......FQEAFLFFFLILKNPLTLCS 54 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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EMBL; 2.72853; CAGA971.1; - EMBL; 2.72853; CAGA9771.1; - SGD; SO003301; CGAG970.1; - SGD; SO003301; CGAG970.1; - Hypothetical protein; Transm TRANSMEM 36 47 SEQUENCE 111 AA; 13603 My Ouery Match SEQUENCE 111 AA; 13603 My Ouery Match A CVRHVLGIGLIVLKNLYFHKNSN 4 CVRHVLGIGLIVLKNLYFHKNSN 1 CTRYFLLLPSYTHPNH 1 12 CTRYFLLLPSYTHPNH 1 12 CTRYFLLLPSYTHPNH 1 12 CTRYFLLLPSYTHPNH 1 16-OCT2001 (Rel. 40, Create 16-OCT2001 (Rel. 40, Last a 10-OCT2001 (Rel. 40, Last a 10-O	Corrections of the control of the co		SULT 1 YG2C_YEAST STANDARD; PRT; 111 AA. P53245; 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) 16-0CT-2001 (Rel. 34). Last annotation update) 17 Saccharomyces cerevisiae (Baker's yeast). Saccharomyces cerevisiae (Baker's yeast). Saccharomycetales; Saccharomycetaceae; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces. NCBL_TAXID-4932; 11] SEQUENCE FROM N.A. Wedler H., Scharfe M., Wedler E., Wambutt R.; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases. This SWISS-PROT entry is copyright. It is produced through a collaborat between the Swiss Institute of Bioinformatics and the EMBL outstatio the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
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"Sequence analysis of a near-subtelomeric 35.4 kb DNA segment on the right arm of bhromosome VII from Saccharomyces cerevisiae carrying the MAL1 locus reveals 15 complete open reading frames, including ZUO1, BGLZ and BIO2 genes and an ABC transporter gene.";
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              Hou S., Wohldmann P., Le T.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: PUTATIVE ODORANT RECEPTOR.
--- SUBCELLULAR LOCATION: Integral membrane protein.
--- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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1-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Very hypothetical 17.3 kDa protein in MALIS-COS6 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 RICFSHLCVIGLVYGTAIIMYVGPRYGNPK---EQKKYLLLFHSLFNPMLNPLICS 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 RRCVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPL---TLCS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .) (POTENTIAL). 8C4F26BBB55C8D7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.8%; Score 59; DB 1; Length 310; 30.4%; Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24; Indels
                                                                                                                                                                                                                                                             PRINTS; PRO0237; GPCKRHODOPSN.
PROSITE; PSO0237; GPCKRHODOPSN.
PROSITE; PSO10237; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Olfaction.
                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                              1 (POTENTIAL)
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                              4 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                        3 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                    InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=S288c / FY1679;
MEDLINE=97245295; PubMed=9090054;
                                                                                                                                                                                                            EMBL; AC005587; AAD05193.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34802 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.4%;
                                                                                                                                                                                                                            OR2A4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                            56
78
99
1119
138
157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         310 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                          HGNC:14729;
    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YG64_YEAST
P53342;
                                                                                                                                                                                                                                                                                                                                                               DOMAIN
TRANSMEM
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                 FRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol. 175:6426-6432(1993).

J. Bacteriol. 175:6426-6432(1993).

-i. FUNCTION: THE BETA SUBUNIT IS RESPONSIBLE FOR THE SYNTHESIS OF L-TRYPTOPHAN FROM INDOLE AND L-SERINE.

-i. CATALYTIC ACTIVITY: L. SERINE.

-i. CATALYTIC ACTIVITY: L. SERINE + 1-(indol.3-yl)glycerol 3-phosphate + 1-(styptophan + glyceraldehyde 3-phosphate + H(2)0.

-i. CAPACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).

-i. PATHWAY: TYPPICAPAN biosynthesis; fifth (last) step.

-i. SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 RCVRHV---LGIGLIVLKNLYFHKNSM-----YPSPKLSSFQEAFLFFFLILKNPLT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning and nucleotide sequence of a putative trpDC(F)BA operon in Buchnera aphidicola (endosymbiont of the aphid Schizaphis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.0%; Score 56.5; DB 1; Length 153; 27.0%; Pred. No. 2.5;
                                              Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
NCBL_TaxID=98794;
                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.; 75652655DBCC01E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tryptophan synthase beta chain (EC 4.2.1.20).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    399 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 20.0%; Score 56.5; DN Best Local Similarity 27.0%; Pred. No. 2.5; Matches 17; Conservative 11; Mismatches
                                                                          -!- SIMILARITY: STRONG, TO YEAST YBR300C.
                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94012512; PubMed=8407819;
Munson M.A., Baumann P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 AA; 17314 MW;
                                                                                                                                                                                                                                                                                                                                      EMBL; Z73078; CAA97326.1; -.
SEQUENCE OF 1-13 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                  S0003525; YGR293C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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85 QP 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
C-C chemokine receptor type 7 precursor (C-C CKR-7) (CC-CKR-7) (MIP-3 beta receptor) (EBV-induced G protein-coupled receptor 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR OF EBV EFFCTS ON B LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6 X CBA; TISSUE=Thymus; MEDLINE=95154835; PubMed=7851893; Schwelckart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr., Sthows T.B., Gray P.W.; "Cloning of human and mouse EBI1, a lymphoid-specific G-protein-coupled receptor encoded on human chromosome 17q12-q21.2."; Genomics 23:643-650(1994).
                                                                                                                                                                                                                                                                                                       Gaps
                                HSSF; FUUSJS; ZWEST.
INTERPROSIS LAWST.
INTERPROSIS TROUGH TEP_SYNCH_Deta.
INTERPROSIS TROUGH TEP_SYNCH_Deta.
PEGREMAS, TIGROROGGS; LTPB; 1.
PROSITE; PSOULGB; TRP_SYNTHASE_BETA; 1.
PROSITE; PSOULGB; TRP_SYNTHASE_BETA; 1.
TYPOCOPHAN DIOSYNTHASE_S; PYRIDOXAL PHOSPHATE; LYABSE.
BINDING 86 86
PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SEQUENCE 399 AA; 44247 MW; DEBED45D2C859C30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000276; GFCR_Rhodpsn.
Pram; PF00001, 7tm_1; 1.
PRINTS; PF00027; GFCRHODDPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50237; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
SIGNAL
STANDAL
STANDA
                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                          DB 1; Length 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-C CHEMOKINE RECEPTOR TYPE 7. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                12; Indels
                                                                                                                                                                                                                                                                                                                                                               14 IVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKN-----PLTLCS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                              20.0%; Score 56.5; Di
36.2%; Pred. No. 6.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  378 AA
                                                                                                                                                                                                                                                                   Local Similarity 36.2%; Pred. No. 6.4; hes 17; Conservative 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OR CMKBR7 OR EBI1 OR EBI1H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Created)
EMBL; Z19055; CAA79500.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L31580; AAA74232.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:103011; Cmkbr7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                         HSSP; P00933; 2WSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CKR7_MOUSE
P47774:
                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EBII)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CKR7_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 VRHVLGIGLIVLK---NLYFHKNSMYPSPK------LSSFQEAFLFF-FLILK 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 VEMILAVGGLIMNTNITVICHKASPMPHPQRRLLASISINFAILSGFQLARNFFLFLVMQ 84
                                                                                                             7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 363;
                                                                                                                                                                                                               19.8%; Score 56; DB 1; Length 378;
                                                                                                                                                                                                                                              22; Indels
                  EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases
                                                                              6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                  ACB1A422CF54AA54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 40.9 kDa protein T09B9.5 in chromosome X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7389680068BAFCB0 CRC64;
   CYTOPLASMIC (POTENTIAL).
                                               5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                               4 CVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLIL 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                               363 AA.
                                                                                                                                                                                                                                Pred. No. 7; 7; Mismatches
                                                                                                                                                                  SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Pred. No. 7.9; 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.6%; Score 55.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
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Hypothetical protein; Transmembrane
                                                                                                                                                                              42941 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40964 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z47070; CAA87342.1; -.
                                                                                                                                                                                                                              32.68;
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                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
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206
247
288
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36
129
378 AA;
                                                                                                                                                                                                                             Similarity
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186
227
268
363 AA;
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153
171
192
220
248
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Q09351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kershaw J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
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DOMAIN
TRANSMEM
                                                                                              DOMAIN
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oshima T., Aiba H., Baba T., Fujihara M., Kanai K., Honjo A., Ikemoto K., Inada T., Itch T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura T., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horluchi T.; Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horluchi T.; Tagami H., Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
                                                                                                                                                                                             STRAIN=K12 / MG1655;
MEDLINE-97426617; PubMed=9278503;
MEDLINE-97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                           Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHÂRACTERIZATION.
MEDLINE-99296569; PubMed-10368134;
Lacroix J.-M., Lanfroy E., Cogez V., Lequette Y., Bohin A.,
                                                                                                                                                                                                                                                                                           "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                   15-771-1998 (Rel. 36, Created)
15-771-1998 (Rel. 36, Last sequence update)
15-771-2001 (Rel. 40, Last annotation update)
Glucans blosynthesis protein mdoC.
                         385 AA
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                         PRT;
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                         STANDARD;
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111
157
193
233
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                                                                                                                                                                                                                                                                                     Shao Y.;
                                                                                                                                                                     NCBI_TaxID=562;
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                                                                                                                                                      Escherichia
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ID MDOC_ECOLI
AC P75920;
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-96068694; PubMed-7479877; Komano H., Fuller R.S.; "Shared functions in vivo of a glycosyl-phosphatidylinositol-linked aspartyl protease, MkC7, and the proprotein processing protease Kex2 in yeast.";
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=S288c / AB972;
Murphy L., Richards C., Harris D., Barrell B.G., Rajandream M.A.,
                                                                                                                                                                                                                                                         01-0cT-1996 (Rel. 34, Created)
1-0cT-1996 (Rel. 34, Last sequence update)
15-10N-2002 (Rel. 41, Last annotation update)
Aspartic proteinase MKC7 precursor (EC 3 4.23.41) (Yapsin 2).
MKC7 OR YBR144C OR YBB358-01C OR YB243.03c.
Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Pungi; Ascomycota; Saccharomycetes;
                                                                                                        1;
                                                                            19.6%; Score 55.5; DB 1; Length 385; 31.1%; Pred. No. 8.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                          Best Local Similarity 31.1%; Pred. No. 8.3;
Matches 14; Conservative 13; Mismatches 17; Indels
                                                    24B869CE8E0224DF CRC64;
                                                                                                                                                 8 VLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPLTL 52
                                                                                                                                                                                                                                                                                                                                                  Sacchāromycetales; Saccharomycetaceae; Saccharomyces. NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 92:10752-10756(1995).
                                                                                                                                                                                                                               596 AA.
            POTENTIAL. POTENTIAL.
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SGD; S000251; MKC7.
InterPro; IPR001461; AspproteaseA1.
InterPro; IPR001969; Aspprotease_site.
                                       POTENTIAL
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                                                     44690 MW;
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EMBL; Z50046; CAA90357.1; --
EMBL; Z54139; CAA90813.1; --
HSSP; P32239; 1YPS.
MEROPS; A01.031; --
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                                                                                                                                                                                                                                 STANDARD;
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 259
294
331
358
239
274
211
311
338
385 AA;
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P53379;
                                          TRANSMEM
SEQUENCE
  TRANSMEM
                                                                                   Query Match
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5

Gaps

4;

15;

Pred. No. 21; 4; Mismatches

41.0%;

Score 54;

51

DB 1; Length 633;

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286 KKNYFDKNSQHIPDPKRRKQNEPGMRLFLVMDEEKNILT 324
                                                                                                      17 KNLYFHKNSMY-PSPKLSSFQEAFLFFFLIL---KNPLT
                      Query Match
Best Local Similarity 41.0
Matches 16; Conservative
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95
101
132
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                                                                                                                                                                                                                                       UL16_HCMVA
P16757;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-S288C / AB972;
Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,
Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
Walsh S.V., Whitchead S.,
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                              ASPARTIC PROTEINASE MKC7.
REMOVED IN MATURE FORM (POTENTIAL).
                                                                                                                                                                                                                                                                         (POTENTIAL)
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                  PROSITE; PS00141; ASP_PROTEASE; 2.
Hydrolase; Aspartyl protease; Glycoprotein; Signal; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 71.0 kDa protein in SGA1-KTR7 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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7B9279E345D4F656 CRC64;
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N-LINKED (GLCNAC...)

POLY-SER.
                                                                                                                                                                                       (GLCNAC...) (GLCNAC...) (GLCNAC...)
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                                                                                                                                                                                                                                                                                                                                 (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 17;
7; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                              A -> T (IN REF. 3).
P -> T (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 54.5;
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Hypothetical protein; Transmembrane.
FRANSMEM 99 118 POTENTIAL.
                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64235 MW;
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39.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Conservative
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PRINTS; PR00792; PEPSIN
                                                          GPI-anchor; Zymogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  596 AA;
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Best Local Similarity
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                                                                                                                CHAIN
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MEDLINE-9026039; PubMed=2161319;

A MEDLINE-9026039; PubMed=2161319;

A Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,

A Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A.,

A Aralysis of the protein-coding content of the sequence of human

The protein Abl69 ";

Curr. Top. Microbiol. Immunol. 154:125-169(1990).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 VLKNLYFHKNSMYP-----SPKLSSFQE------AFLFFFLILKNPL 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Mismatches 16; Indels 24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26147 MW; B72F2C241C569967 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC...)
                                                                                                                                                                            Human cytomegalovirus (strain AD169).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
                                         01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-FBB-1991 (Rel. 17, Last annotation update)
Hypothetical protein UL16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC.
230 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 34, Created)
(Rel. 34, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 53;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X17403; CAA35448.1; -. PIR; S09778; S09778.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.7%;
23.8%;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                           NCBI_TaxID=10360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQP5_HUMAN
P55064;
01-OCT-1996 (
01-OCT-1996 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
AQP5_HUMAN
ID AQP5_HU
AC P55064;
DT 01-OCT-
DT 01-OCT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 LSIGLSVTLGHLVGIYFTGCSMNPARSFGPAVVMNRFSPAHWVFWVGPIVGAVLAAILYF 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 12;
8; Mismatches 17; Indels 26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=96224064; PubMed=8621489;
Lee M.D., Bhakta K.Y., Raina S., Yonescu R., Griffin C.A.,
Lee M.D., Bhakta K.Y., Raina S., Yonescu R., Griffin C.A.,
Copeland N.G., Gilbert D.J. Jenkins N.A., Preston G.M., Agre P.;
The human Aquaporin-5 gene. Molecular characterization and
chromosomal localization.";
J. Biol. Chem. 271:8599-8604(1996).
I. FORKEY CHEMS AMATER-SPECIFIC CHANNEL. IMPLICATED IN THE
GENERATION OF SALIVA, TEARS, AND PULMONARY SECRETIONS.
I. SUBCELLULAR LOCATION: Integral membrane protein.
I. SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY (TC 1.A.8).
                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTIONAGEMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.7%; Score 53; DB 1; Length 265; 27.1%; Pred. No. 12:
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01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
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EMBL; U46566; AAC50474.1; JOINED.
EMBL; U46567; AAC50474.1; JOINED.
EMBL; U46568; AAC50474.1; JOINED.
HSSP; P29972; 1H61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0783; MINTRINSICP.
ProDom; PD000295; MIP_family; 1.
TIGREAMS; TIGRO0861; MIP; 1.
PROSITE; PS00221; MIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000425; MIP_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28292 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transport; Transmembrane.
DOMAIN 1 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HGNC:638; AQP5.
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162
183
206
227
124
125
25 AA;
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223 YLLFPNSLSL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43 FLILKNPLTL 52
                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genew; HGNC: (
MIM; 600442;
              Aquaporin 5.
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DOMAIN
TRANSMEM
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TRANSMEM
DOMAIN
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TRANSMEM
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δλ
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RESULT 12

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

Rad Squros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

Rad Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

Rad Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

Rad Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

Rad Gollins M., Connor R., Cronin A., Davis P., Fictwell T., Fraser A.,

Rad Gollins M., Connor R., Cronin A., Davis P., Hidalgo J., Hodgson G.,

Rad Holroyd S., Honraby T., Howarth S., Hunckle E.J., Hunt S., Jagels K.,

Amoney P., Noules S., Mungall K., Murphy L., Niblett D., Odell C.,

Rad Oliver K., O'Neil S., Pearson D., Quall M.A., Rabbinowitsch E.,

Rad Cliver K., O'Neil S., Ronders D., Seeger K., Sharp S.,

Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

Radlton J., Simmond M., Squares R., Squares S., Stevens K.,

Radlton K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whithehead S.,

Radlton J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Radlelon J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Radlelon J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Radlelon J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Radlelon J., Langer I., Beck A., Iehrach H., Reinhardt R., Pohl T.M.,

Borzym K., Langer I., Beck A., Iehrach H., Reinhardt R., Pohl T.M.,

Radlibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,

Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,

Lucas M., Rochet M., Gallardin C., Paulsen I., Pottashkin J.,

Rad Daga R. R., Cruzado L., Jimenez J., Sanchez M., Galzon A., Thode G.,

Rad Daga R. R., Cruzado L., Jimenez D., Arnstrong J., Forsburg S.L.,

Rad Daga R. R., Cruzado L., Jimenez D., Ranstrong J., Rochet M., Garzon P.,

Rad Daga R. R., Cruzado L., Jimenez D., Ranstrong J., Rochet M., Garzon P.,

Rad Daga R. R., Cruzado L., Jimenez D., Ranstrong J., Pottashkin J.,

Rad Prophysiki G.V., Ussery D., Barrell B.G., Nurse P.,

                                                                                                                                                                                                                                                                                                                                         MEDITALE 93223713; PubMed=8467814;
Molz L., Beach D.; "Characterization of the fission yeast mcs2 cyclin and its associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN C SUBFAMILY.
                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                         Cyclin mcs2 (Mitotic catastrophe suppressor 2)
                                              01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
322 AA
                                                                                                                                                                          pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00134; cyclin; 1.
SMARY; SM00134; cyclin; 1.
TRRFAMs, TICRFON5; ccll; 1.
PROSITE; PS00292; CYCLINS; FALSE_NEG.
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL441603; CAC08541.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; S59895; AAB26193.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P51946; 1KXU.
InterPro; IPR005258; Ccll.
InterPro; IPR004366; Cyclin.
                                                                                                                                                                                                                                                                                                                                                                                                                    protein kinase activity.";
EMBO J. 12:1723-1732(1993).
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S35380; S35380.
                                                                                                                                                                                                                                                    Schizosaccharomyces.
                                                                                                                                                  MCS2 OR SPBP16F5.02.
                                                                                                                                                                            Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                         NCBI_TaxID=4896;
     CGM2_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=972
                            P36613;
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VP4B_VACCC
           VP4B_VACCV
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                                 δλ
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                                                        ö
                                                                                                                                                                                                                                                                                                                                  STRAIN=CV. Texas Marker 1; TISSUE=Fiber;
Shin H., Brown R.M. Jr.;
"Two CDNA sequences for the adenine nucleotide translocator, CANT1 and CANT2, from cotton fibers (Gossypium hirsutum).";
(In) Plant Gene Register PCR97-130.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                    Gossypium hirsutum (Upland cotton).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADP.ATP carrier protein 1, mitochondrial precursor (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
                                                                                                                                                                                                                                                                                                                                                                                                     inner membrane (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MITOCHONDRION (BY SIMILARITY). ADP, ATP CARRIER PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.7%; Score 53; DB 1; Length 386;
                                  18.7%; Score 53; DB 1; Length 322,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 IGLIVLKNLYFHKNSMYPSPK----LSSFQEAFLFFFL---ILKNPLTLCS
                                                         18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A05F76C73FECDEE6 CRC64;
Cyclin; Cell cycle; Cell division; Nuclear protein. SEQUENCE 322 AA; 37673 MW; 09B8DDB46563727C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                             8; Mismatches
                                             32.4%; Pred. No. 15; ive 5; Mismatches
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                                                                               7 HVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFL 40
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Interpro; IPR001993; Mitoch_carrier.
                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF006489; AAB72047.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.3%;
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                                                         11; Conservative
                                                                                                                                                              STANDARD;
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386
107
170
212
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hes 17; Conserv
           322 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 386 AA;
                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3635;
                                                                                                                                                              ADT1_GOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                   Query Match
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                                                         Matches
                                                                                                                                       RESULT 13
ADT1_GOSHI
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                                                                                                                                                                                                                                                                                                                                                                                    and nucleotide sequence
the precursor of the major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Gen. Virol. 72:411'416(1991).
-!- FUNCTION: PRECURSOR FOR ONE OF THE TWO MOST ABUNDANT STRUCTURAL COMPONENT OF THE VIRION (MAJOR CORE PROTEINS 4A AND 4B).
                                                                                                                                                                                                      Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      van Slyke J.K., Franke C.A., Hruby D.E.; "Proteolytic maturation of vaccinia virus core proteins: identification of a conserved motif at the N termini of the 4b and 25K virion proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Major core protein P4b precursor (Virion core protein P4b).
                                                01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
16-CCT-2010 (Rel. 40, Last annotation update)
Major core protein P4b precursor (Virion core protein P4b).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.7%; Score 53; DB 1; Length 643; 29.5%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SEP-1989) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q -> N (IN REF. 2).
; 6F073332BAFD0E59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     339 LFGIKLPALENAYVHGDTYSLIQQLYEFRKVKSYNYMLLVNRLT 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAJOR CORE PROTEIN P4B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 VLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                           "Transcriptional and translational mapping analysis of a vaccinia virus gene encoding core polypeptide 4b.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 62-70.
MEDLINE=91132139; Pubmed=1993877;
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=86062913; PubMed=2999438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    643 AA; 72498 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A03871; FOVZZW.
InterPro; IPR004972; Pox_P4B.
Pfam; PF03292; Pox_P4B; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M11079; AAA48298.1; -. EMBL; M27914; AAA48303.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Virol. 56:830-838(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
SEQUENCE OF 1-201 FROM N.A.
                                                                                                                                                                                   Vaccinia virus (strain WR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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  STANDARD;
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Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                   Rosel J., Moss B.;
                                                                                                                                                                                                                                                         NCBI_TaxID=10254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Core protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    van Meir E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VP4B_VACCC
VP4B_VACCV
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                                                                                                                                                                                                                                                                                   *Appendix to 'The complete DNA sequence of vaccinia virus'.";
Virology 179:517-563(1990).
-!- FUNCTION: PRECURSOR FOR ONE OF THE TWO MOST ABUNDANT STRUCTURAL
COMPONENT OF THE VIRION (MAJOR CORE PROTEINS 4A AND 4B).
Vaccinia virus (strain Copenhagen).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                           SEQUENCE FROM N.A.
BEDLINE-91021027; PubMed=2219722;
Goebbel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
Paoletti E.;
                                                                                                                                                                                                                                                   Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P., Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 18.7%; Score 53; DB 1; Length 644; Best Local Similarity 29.5%; Pred. No. 29; Matches 13; Conservative 11; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
MAJOR CORE PROTEIN P4B.
76CC2ED6781F88A2 CRC64;
                                                                                                                                                                        "The complete DNA sequence of vaccinia virus."; Virology 179:247-266(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROPEP 1 61 BY CHAIN 62 644 MS SEQUENCE 644 AA; 72624 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, M35027; AAA48118.1; -.
PIK; E42517, FOVZE,
InterPro; IPR004972; POX_P4B.
Pfam; PF03292; POX_P4B; I.
                                                        NCBI_TaxID=10249;
                                                                                                                                                                                                                                 COMPLETE GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Core protein.
PROPEP
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Search completed: November 21, 2002, 13:41:50 Job time : 13 secs

8 VLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPLT 51

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Gaps

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November 21, 2002, 13:40:47; Search time 29 Seconds
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                 OM protein . protein search, using sw model
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(without alignments) 383.674 Million cell updates/sec US-09-776-724A-142

I MRRCVRHVLGIGLIVLKNLY......FQEAFLFFFLILKNPLTLCS 54 Perfect score: Sequence:

671580 seqs, 206047115 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp_unclassified:* sp_human:*
sp_invertebrate:*
sp_mammal:* sp_vertebrate:* sp_bacteriap:* sp_archea:*
sp_bacteria:*
sp_fungi:* sp_organelle:* rodent: * sp_rvirus:* sp_plant:* sp_virus:* SPTREMBL_21:* sp_phage: sb_mhc: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

026431 methanobact 09nqn0 homo sapien 09i8c2 xenopus lae Q9stw2 arabidopsis 082159 populus nig 09bb39 dichaea mur Q8zhg6 yersinia pe Q9bb34 cryptarrhen Q9c4y2 sulfolobus 024437 oryza longi O9bb38 dichaea neg 024788 echinococcu 08ss65 encephalito Q9bb33 chondrorhyn 095bp4 pescatorea 09bb32 pescatorea Description SUMMARIES 024437 082159 09BB39 Q9NQN0 Q9I8C2 Q9STW2 98ZHG6 Q9BB32 **095BP4** Q9BB33 **09BB38** Q9C4Y2 1 1 1 1 Query Match Length DB 20.5 20.5 20.5 20.5 20.5 20.5 20.5 20.3 20.3 Score 58.5 58.5 58 58 58 58 58 58 57 57 Ş.

Q94736 stomoxys ca O93552 carassius a Q8wf21 bhutanitis Q9yx20 melanoplus Q8ht5 methanosarc Q9bb37 warrea warr Q91p15 arabidopsis Q92t57 arabidopsis Q92t57 arabidopsis Q92t67 arabidopsis Q9xed arabidopsis Q9xed archetobact Q9xed acropyrum p Q9b6q1 eulachnus s Q9xers caenorhabdi Q956q1 eulachnus s Q9xers caenorhabdi Q956q2 archaeoglob Q966q3 archaeoglob Q966q3 archaeoglob Q96ma5 homo sapien Q8x16 escherichia Q94x16 escherichia Q93t47 rice black Q8uz09 rice black Q8uz09 rice black Q8uz09 rice black Q9baz7 soterosanth Q9baz7 soterosanth Q9baz7 kegeliella Q9baz7 staphylococ Q9h07 staphylococ Q9n5i3 caenorhabdi
094736 093552 08WF21 2 Q9YVZ0 08THT5 09BB37 09BB37 092LPL5 092DD2 092DD2 092BG01 098BG01 098BA27 0817D1 098BA27 0817D1 099BA25 099BA27 0914N7 0817D1 099BA27 0914N7
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ALIGNMENTS

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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 17, Last annotation update)
11-201 (TrEMBLrel. 17, Last annotation update)
Hypotherical 45.7 kDa protein.
1722A6.150 OR AT4G24320
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Limmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
BEVARD M., ZIMMETMARD W., Grueneisen A., Wambutt R., Bancroft I.,
Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                 EU Arabidopsis sequencing project; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ET Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL078637; CAB45067.1;
EMBL; AL161861; CAB75942.1;
InterPro: JPR002203; Intein.
PROSITE: PS00881; PROTEIN_SPLICING; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 395 AA; 45690 MW; EA8CE0F16E1E806D CRC64;
                                        395 AA.
                                        PRT;
                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                 Q9STW2
                                                     Q9STW2;
RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-DELINE—98037514; PubMed-9371463; Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J., Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Glason R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Praphakar S., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; Complete genome sequence of Methanobacterium thermoautctrophicum deltaH: functional analysis and comparative genomics.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 RRCVRHVLGIGL------39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 17, Last annotation update)
01-UNN-2000 (TrEMBLrel. 17, Last annotation update)
011005H11.1 (7 transmembrane receptor (Rhodopsin family) (Olfactory receptor like) (Fragment).
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                    4;
                                                                                                                                                                                                                                                                                                   Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 60; DB 17; Length 221;
Pred. No. 5.6;
8; Mismatches 15; Indels '
                                                                                     4 CVRHVLGIGLIVLKNLYFHKNSMYPSPKLSS----FQEAFLFFFLILKNPL 50
 Score 63; DB 10; Length 395;
Pred. No. 3.9;
8; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Bacteriol. 179:7135-7155(1997).

EMBL, AE000818; AAB8487.1; -.

Interpro; IPR001173; Glycos_transf_2.

Pfam, PF00535; Glycos_transf_2? 1.

Transferase; Glycosyltransferase; Complete proteome.

SEQUENCE 221 AA; 24710 MW; 96B0E95F98081A09 CRC64;
                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) MANNOSYLTRANSFERASE.
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                                                                                                                                                                                         PRT;
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30.9%;
          22.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                         17; Conservative
                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                            01-JAN-1998 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 IFRTLVLE 218
                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 LFFFLILK 47
                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-DELTA H;
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             Query Match
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Gaps
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Receptor kinase-like protein.
0ryza longistaminata (Long-staminate rice).
0ryza, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
Kanopus Ametazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                   200 RICFSHLCVIGLVYGTAIIMYVGPRYGNPK---EQKKYLLLFHSLFNPMLNPLICS 252
                                                                                                                                                                                  2 RRCVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPL---TLCS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.7%; Score 58.5; DB 13; Length 325; 28.3%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 CVRHVLGIGLIVLKNLYFHKNSMYP---SPKLSSFQEAFLFFFLILKNPLTLC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Two classes of olfactory receptors: molecular and functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28; Indels
                                                                                                                       20.8%; Score 59; DB 4; Length 272; 30.4%; Pred. No. 9.2;
                                                                                                                                                        24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             325 AA; 37075 MW; 94CDE3DC322C97A4 CRC64;
                                                                                   NON_TER 1 1 1
SEQUENCE 272 AA; 30452 MW; 4FF5CF18077574CD CRC64;
                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0237; GPCTRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               612 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Mismatches
                                                                                                                                                          9; Mismatches
          InterPro: IPR000276; GPCR_Rhodpsn.
Pfam: PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AJ250752; CAC00723.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=IRBB21;
MEDLINE=96106403; PubMed=8525370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-OLFACTORY EPITHELIUM;
Mezler M., Breer H.;
                                                                                                                                              30.4%;
                                                                                                                                                                                                                                                                                                                                                                                         Olfactory receptor class I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
EMBL; AL135904; CAB99212.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                              Best Local Similarity 30.49
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 15; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM. N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor.
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                                                                                                                                 Query Match
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Song W.Y., Wang G.L., Chen L.L., Kim H.S., Pi L.Y., Holsten T., Gardner J., Wang B., Zhai W.X., Zhu L.H., Fauquet C., Ronald P.; "A receptor kinase-like protein encoded by the rice disease resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Populus nigra (Lombardy poplar).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids [; Malpidhiales; Salicaceae; Populus.
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                      5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nishiguchi M.;
"A cDNA clone encoding cytosolic phosphoglycerate kinase 2 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                                                                                                                                                     20.7%; Score 58.5; DB 10; Length 612; 38.3%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bibmitted (CCT-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + 3-PHOSPHO-D-GLYCERATE = ADP + 3-PHOSPHO-D-GLYCEROYL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1-SUBULIT: MONDER. (BY SIMILARITY).
-1-SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.
BENEL; AB010411; BAA33802.1; -.
HSSP; P18912; 1PHP.
InterPro; IPR001576; PGK.
Pfam; PF00162; PGK; 1.
PRINTS; PR00477; PHGLYCKINASE.
PROSITE; PS00111; PGLYCERATE_KINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 20.5%; Score 58; DB 10; Length 401; 1 Similarity 29.5%; Pred. No. 18; 13; Conservative 11; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                   19; Indels
                                                                                                                                                                                                                                                                                                                                                         1 MRRCVRHVLGIGLIVLKNLYFHKNSM---YPSP--KLSSFQEAFLFF 42
                                                                                                                                                                                                                                                         612 AA; 66380 MW; 9BE54BBB4242A91F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycolysis; Kinase; Transferase.
SEQUENCE 401 AA; 42669 MW; 79B095EE6B1A9DA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MRRCVRHVLGIGLIVLKNLYFHKNSMYPSP----KLSSFQEAFL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Phosphoglycerate kinase (EC 2.7.2.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                           401 AA.
                                                                                                                                                                                                                                                                                                                5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                       MEDLINE=97432142; PubMed=9286106;
                                                    Science 270:1804-1806(1995).
                                                                                                                                                                                                                                                                                           watches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                SMART; SM00370; LRR; 17
                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                               STRAIN=IRBB21;
                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                               Kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                     082159
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RESULT 7

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INTRONS (BY SIMILARITY).
----SMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRONS.
                                                                                                                                              Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae; Epidendroideae; higher Epidendroideae; Maxillarieae; Zygopetalinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Williams N.H., Chase M.W., Fulcher T., Whitten M.W.; "Molecular systematics of the Oncidiinae based on evidence from four DNA sequence regions: expanded circumscriptions of Cyrtochilum, Erycina, Otoglossum, and Trichocentrum, and a new genus (Orchidaceae)..;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae; Epidendroideae, higher Epidendroideae; Maxillarieae; Zygopetalinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||::| || ::| || ::|
262 LILMKKWKFHLVNFWQSYFHFWFQPYRIHIKKLPNYSFSFLGYFSIVLKNPLVV 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Mismatches 13; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lindleyana 16:113-139(2001).
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
INTRONS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 LIVLKNLYFHKNSMYPS------PKLSSFQEAFL-FFFLILKNPLTL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.5%; Score 58; DB 8; Length 440; 29.6%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        440 AA; 52685 MW; CFFBAF87755FF9E5 CRC64;
                                                             (TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                     Probable intron maturase (Maturase K) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probable intron maturase (Maturase K) (Fragment).
                 440 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 446 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00436; PEROXIDASE_2; UNKNOWN_1. Chloroplast; mRNA processing.
                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF239415; AAK31812.1; -.
InterPro; IPR000442; Intron maturse2.
InterPro; IPR002865; Matk.N.
InterPro; IPR002016; Peroxidase.
                                             01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; MatK_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
es 16; Conserv
                                                                                                                                                                                                                NCBI_TaxID=125110;
                                                                                                                     Dichaea muricata.
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=125160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          440
                                                                        01-MAR-2002
                                                                                                                                    Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pescatorea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                             Q9BB39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON TER
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              09BB39
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Q9BB39
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Q9BB33;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Whitten M., Williams N.H., Chase M.W.;
"Tribal and subtribal relationships of Maxillarieae (Orchidaceae) with special emphasis on Stanhopeinnae: Combined molecular evidence."; submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
i- PUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTRONS (BY SIMILARITY).

1. SIMILARITY: WITH CORRESPONDING ORP IN OTHER PLANT CHLOROPLASIS, AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY MITOCHONDRIAL INTRONS.
-i- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS, AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
Epidendroideae; higher Epidendroideae; Maxillarleae; Zygopetallnae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 LIVLKNLYFHKNSMYPS------PKLSSFQEAFL-FFFLILKNPLTL 52
                                                                                                                                                                                                            269 LILMKKWKFHLVNFWQSYFHFWFQPYRIHIKKLPNYSFSFLGYFSIVLKNPLVV 322
                                                                                                                                                                                                13 LIVLKNLYFHKNSMYPS-------FKLSSFQEAFL-FFFLILKNPLTL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.5%; Score 58; DB 8; Length 452; 29.6%; Pred. No. 20; tive 11; Mismatches 13; Indels
                                                                                                                                                   DB 8; Length 446;
                                                                                                                                                                          13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              452 AA; 53955 MW; A978F3CF6B10BA25 CRC64;
                                                                                                                               446 AA; 53294 MW; BC07C941362FBB6E CRC64;
                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Probable intron maturase (Maturase K) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1
                                                                                                                                                                           11; Mismatches
                                                                                                                                                                                                                                                                               452 AA.
                                                                                                                                                   Score 58; DB Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF239422; AAK31819.1; -.
Interpro; IPR000005; HTHAraC.
Interpro; IPR000442; Intron_maturse2.
                                 EMBL, AF350662, AAK77122.1; --
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR012866, Matk_N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; Matk_N; 1.
                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel, 17, Created)
01-JUN-2001 (TrEMBLrel, 17, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002866; MatK_N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; MatK_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chloroplast; mRNA processing.
                                                                                              Chloroplast; mRNA processing.
                                                                                                                                                      20.5%;
29.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                  Local Similarity 29.69 ies 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       452
                                                                                                                      446
                                                                                                                                                                                                                                                                                                                                                              Pescatorea lehmannii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=125160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                     446
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                                                                                                                                                                                                                                                                                                                                                                         chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                      Pescatorea
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SEQUENCE
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NON_TER
SEQUENCE
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                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                09BB32
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                                                                                                                                                                              Matches
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Q9BB33

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Whitten M., Williams N.H., Chase M.W.;

Whitten M. Williams N.H., Chase M.W.;

RT Special emphasis on Stanhopeinae: Combined molecular evidence.";

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

C. I. SUMLAN PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II

INTRONS (BY SIMLARITY).

C. I. SIMLARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,

AND REGIONS OF SIMLARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY

MITOCHONDRIAL INTRONS.

C. MITOCHONDRIAL INTRONS.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Whitten M., Williams N.H., Chase M.W.; Whitten M., Williams N.H., Chase M.W.; Tribal and subtribal relationships of Maxillarieae (Orchidaceae) with special emphasis on Stanhopeinae: Combined molecular evidence."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTRONS (BY SIMILARITY).

-1. SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
Epidendroideae; higher Epidendroideae; Maxillarieae; Zygopetalinae;
                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
Epidendroideae; higher Epidendroideae; Maxillarleae; Zygopetallnae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 LIVLKNLYFHKNSMYPS------PKLSSFQEAFL-FFFLILKNPLTL 52
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Pred. No. 20;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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                                                                                                                                                         Probable intron maturase (Maturase K) (Fragment).
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11; Mismatches
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                                                                                                                                                                                                                                                                        Chondrorhyncha reichenbachiana.
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Query Match
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Q9BB34
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Q8ZHG6
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                                                                                                                                           14;
                                                                                                                                                                            184 LILMKKWKFHLVNFWQSYFHFWFQPYRIHIKKLPNYSFSFLGYFSIVLKNPLVV 337
                                                                                                                                                            13 LIVLKNLYFHKNSMYPS------PKLSSFQEAFL-FFFLILKNPLTL 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 LGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNP-----LTLCS 54
                                                                                                                    20.5%; Score 58; DB 8; Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Match 20.5%; Score 58; DB 5; Length 559; Local Similarity 33.3%; Pred. No. 25; Losservative 7; Mismatches 19; Indels
                                                                                                                                          13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ECUO4_0310.
Encephalitozoon cuniculi.
Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
Cyclophyllidea; Taeniidae; Echinococcus.
NCBI_TaxID=6210;
                                                                                              486 AA; 58096 MW; EAB0B4C50058B5CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00935; BAND41.
SMART; SM00295; B41; 1.
PROSITE; PS50057; BAND_41_3; 1.
SEQUENCE 559 AA; 65213 MW; 4781F013BAD92DA5 CRC64;
                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
265 protessome regulatory subunit 4.
                                                                                                                                       11; Mismatches
                                                                                                                                                                                                                                         559 AA
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          InterPro; IPR002866; Matk.N.
InterPro; IPR022016; Peroxidase.
Pfam; PP01348; Intron_maturas2; 1.
Pfam; PF01824; Matk.N; 1.
PROSITE; PS00436; PEROXIDASE_2; UNKNOWN_1.
                                                                                                                                Pred. No. 22;
InterPro; IPR000442; Intron_maturse2
                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                          PRT;
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                                                                                                                             Best_Local Similarity 29.6%;
Matches 16; Conservative 1
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STRAIN-CATTLE ISOLATE;
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SEQUENCE
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                                                                                                                            P SEQUENCE.

X MEDLINE-21576510; PubMed-11719806;

X Actinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,

RA Prensier G., Barbe V., Peyretaillade E., Brottler P., Wincker P.,

RA Debac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,

RA Weissenbach J., Vivares C.P.;

RT Genome sequence and gene compaction of the eukaryote parasite

RT Encephalitozoon cuniculi.";

RL Nature 414:450-453(2001).

DR EMBL; AL590444; CAD25218 1;

S SEQUENCE 795 AA; 89126 MW; 6654367B915F8516 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDINES-214 Grovar Orientals;
MEDINES-214 (19413; PubMed=11566360;
MEDINES-214 (19413; PubMed=11566360;
MEDINES-214 (19413; PubMed=11566360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamilin N., Hollcoyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,
"Genome sequence of Versinia pestis, the causative agent of plague.",
Mature 413:523-557(2001).
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Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.5%; Pred. No. 34;
tive 6; Mismatches 11; Indels
                         Genoscope; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR000130; Zn_MTpeptdse.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
Hypothetical protein; Complete proteome.
SEQUENCE 170 AA; 19923 MW; 5C172226B3962FB0 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein YP00932.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17; Conservative
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                                                                                                                  SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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STRAIN-GB-M1;
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                                                                                                                                                 Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
Epidendroideae; higher Epidendroideae; Maxillarieae; Zygopetalinae;
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503 Aa; 60144 MW; C9C114E8B9A03000 CRC64;
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                      Probable intron maturase (Maturase K) (Fragment).
                                                                                                              Cryptarrhena lunata.
                                                                                                                                                                                                                                                                                              Cryptarrhena.
NCBI_TaxID=125104;
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SEQUENCE
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Search completed: November 21, 2002, 13:42:27 Job time : $33\ \mathrm{secs}$

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Sequence 142, App
Sequence 142, App
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Sequence 6555, Ap
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1 MRRCVRHVLGIGLIVLKNLY......FOEAFLFFFLILKNPLTLCS 54
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7.9712_7.ppad_710_5.004B.ppp; *
7.9712_5.ptodata_1/ppad_7105(0.00B.ppp; *
7.9712_6.ptodata_1/ppad_7105(0.00B.ppp; *
7.9712_6.ptodata_1/ppad_7108B_0.00B.ppp; *
7.9712_6.ptodata_1/ppad_71089B_0.00B.ppp; *
7.9712_6.ptodata_1/ppad_71010_0.00B.ppp; *
7.9712_6.ptodata_1/ppad_71000B_0.00B.ppp; *
7.9712_6.ptodata_1/ppad_7100B_0.00B.ppp; *
7.9712_6.ptodata_1/ppad_7100B_0.00B_0.00B.ppp; *
7.9712_6.ptodata_1/ppad_7100B_0.00B_0.00B_0.00B_0.00B_0.00B_0.00B_0.00B_0.00B_0.00B_0.00B_0.00B_0.00B_0.00B_0.00B_0.00B_0.00B_0.00B_0.00B_0.00B_0.00B_0.00B
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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'Cgn2_5/ptodata/1/paa/PCTUS_COMB.pep:*
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5 US-09-229-982-142
0 US-09-668-142
1 US-09-776-724A-142
PCT-US01-01334-6555
1 US-09-764-874-6555
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Sequence 164, App
Sequence 218, App
Sequence 475, Ap
Sequence 5353, Ap
Sequence 5353, Ap
Sequence 11072, A
Sequence 29013, A
Sequence 2013, A
Sequence 30438, A
Sequence 9686, Ap
Sequence 9686, Ap
Sequence 9686, Ap
Sequence 3686, Ap
Sequence 3686, Ap
Sequence 36767, A
Sequence 35767, A
Sequence 59521, A
Sequence 35040, A
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Sequence 58, Appl
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                                                                                                     US-09-764 891-4675
US-09-764 891-4675
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US-09-708-427-29014
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US-09-713-8586-35
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SERERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: 64 Human Secreted Proteins
FILE REFERENCE: P2011PCT
CURRENT APPLICATION NUMBER: PCT/US98/14613
CURRENT FILING DATE: 1998-07-15
EARLIER FILING DATE: 1997-07-16
NUMBER OF SED ID NOS: 178
SOFTWARE: Patentin Ver: 2.0
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PCT-US98-14613-142
 PCT-US98-14613-142
SEQ ID NO 142
LENGTH: 54
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; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
TITLE OF INVENTION: 64 Human Secreted Proteins
                                                                      APPLICANT: Rosen et al.
TITLE OF INVENTION: 64 Human Secreted Proteins
                                                                                                                                                    CURRENT FILING DATE: 1999-01-14

CURRENT FILING DATE: 1999-01-14

EARLIER APPLICATION NUMBER: US/09/229,982

CURRENT FILING DATE: 1999-01-14

EARLIER PAPLICATION NUMBER: 1997-07-16

EARLIER PAPLICATION NUMBER: 1997-07-22

EARLIER PAPLICATION NUMBER: 1997-07-22

EARLIER PAPLICATION NUMBER: 1997-07-22

EARLIER PAPLICATION NUMBER: 1997-07-22

EARLIER PAPLICATION NUMBER: 1997-08-18

EARLIER PILING DATE: 60/053,442

EARLIER PAPLICATION NUMBER: 1997-08-18

EARLIER PAPLICATION NUMBER: 1997-08-18

EARLIER PILING DATE: 60/055,985

EARLIER PILING DATE: 60/055,986

EARLIER PILING DATE: 60/055,986

EARLIER PILING DATE: 60/055,986

EARLIER FILING DATE: 6
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EARLIER FILING DATE: 60/055,683
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 142
Sequence 142, Application US/09229982 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
                                                                                                                                             FILE REFERENCE: PZ011P1
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100.0%; Pred. No. 1.4e-27;
tive 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: ROSen et al.
TITLE OF INVENTION: 64 Human Secreted Proteins
FILE REFERENCE: P2011
CURRENT FAPLICATION NUMBER: US/09/776,724A
CURRENT FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/180,909
                CURRENT APPLICATION NUMBER: US/09/669,688 CURRENT FILING DATE: 2000-09-26
                                                                                                    PRIOR FILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: PCT/US98/14613
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/052,661
PRIOR FILING DATE: 1997-07-16
                                                                                                                                                                                                                                                                                         PRIOR PELLICALION NUMBER: 60/052,871
PRIOR FILING DATE: 1997-07-16
PRIOR FILING DATE: 1997-07-16
PRIOR FILING DATE: 1997-07-16
PRIOR PLICATION NUMBER: 60/052,874
PRIOR PLICATION NUMBER: 60/052,873
PRIOR PLILING DATE: 1997-07-16
PRIOR PLILING DATE: 1997-07-16
PRIOR PLILING DATE: 1997-07-16
PRIOR PLILING DATE: 1997-07-22
PRIOR PLILING DATE: 1997-08-18
PRIOR PRILING DATE: 1997-08-18
PRIOR PLILING DATE: 1997-08-18
                                                                          PRIOR APPLICATION NUMBER: US/09/229,982
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PRIOR APPLICATION NUMBER: 60/055,946
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PRIOR APPLICATION NUMBER: 60/055,683
NUMBER OF SEQ ID NOS: 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Ver. 2.0
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FILE REFERENCE: PZ011P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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US-09-776-724A-142
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LENGTH: 54
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PRIOR APPLICATION NUMBER: 60/219, 065
PRIOR FILING DATE: 2000-01-31
PRIOR PLICATION NUMBER: 60/214, 886
PRIOR FILING DATE: 2000-02-04
PRIOR PRICKATION NUMBER: 60/217, 487
PRIOR APPLICATION NUMBER: 60/217, 487
PRIOR APPLICATION NUMBER: 60/217, 496
PRIOR PLING DATE: 2000-07-11
PRIOR PLING DATE: 2000-07-12
PRIOR PRILING DATE: 2000-07-13
PRIOR PLING DATE: 2000-07-14
PRIOR PRILING DATE: 2000-07-14
PRIOR PRILING DATE: 2000-07-14
PRIOR PRILING DATE: 2000-08-14
PRIOR PRILING DATE: 2000-09-14
PRIOR PRILING DATE: 2000-09-19
PRIOR PRILING DATE: 2000-09-29
PRIOR PRILING DATE: 2000-09-29
PRIOR PRILING DATE: 2000-09-29
PRIOR PRILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/236,369
PRIOR PRILING DATE: 2000-09-29
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PRIOR APPLICATION UNMBER: 60/229,343
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229,345
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Best Local Similarity 100.0%; Score 283; DB 21; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.4e-27;
Matches 54; Conservative 0; Mismatches 0; Indels
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCIOLOGT
CURRENT APPLICATION NUMBER: PCT/US01/01334
CURRENT FILING DATE: 2001-01-17
PRIOR FILING DATE: 2000-02-08
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 1090-01-14
PRIOR FILING DATE: 1999-01-14
PRIOR PELICATION NUMBER: 09/229,982
PRIOR FILING DATE: 1999-07-15
PRIOR PELICATION NUMBER: 60/052,871
PRIOR PELICATION NUMBER: 60/052,872
PRIOR PLILING DATE: 1997-07-16
PRIOR PELICATION NUMBER: 60/052,871
PRIOR APPLICATION NUMBER: 60/052,871
PRIOR PELICATION NUMBER: 60/052,874
PRIOR PELING DATE: 1997-07-16
PRIOR PELING DATE: 1997-07-22
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PRIOR APPLICATION UNBER: 60/055,725
PRIOR APPLICATION NUMBER: 60/055,985
PRIOR FILING DATE: 1997-08-18
PRIOR FILING DATE: 1997-08-18
PRIOR FILING DATE: 1997-08-18
PRIOR FILING DATE: 1997-08-18
PRIOR PILING DATE: 1997-08-18
PRIOR PILING DATE: 1997-08-18
PRIOR PILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: 60/055,361
PRIOR FILING DATE: 1997-08-18
PRIOR PILING DATE: 1997-08-18
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PRIOR FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: 60/055,946
PRIOR FILING DATE: 1997-08-18
PRIOR PRIOR DATE: 1997-08-18
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SEQ ID NO 142
LENGTH: 54
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PRIOR FILING DATE: 2000-09-01
PRIOR PELICATION UNDREES: 60/229, 287
PRIOR PELICATION UNDREES: 60/229, 513
PRIOR PELICATION UNDREES: 60/229, 513
PRIOR PELICATION UNDREES: 60/229, 513
PRIOR PELICATION UNDREES: 60/221, 413
PRIOR PELICATION UNDREES: 60/221, 413
PRIOR PELICATION UNDREES: 60/221, 413
PRIOR PELICATION UNDREES: 60/221, 039
PRIOR PELICATION UNDREES: 60/231, 039
PRIOR PELICATION UNDREES: 60/231, 039
PRIOR PELICATION UNDREES: 60/231, 039
PRIOR PELICA DATE: 2000-10-02
PRIOR PELICATION UNDREES: 60/231, 037
PRIOR PELICATION UNDREES: 60/232, 037
PRIOR PELICATION UNDREES: 60/249, 213
PRIOR PELICATION UNDREES: 60/249, 229
PRIOR PELICATION UNDREES: 60/249, 229
PRIOR PELICATION UNDREES: 60/249, 229
PRIOR PELI

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1 MRRC-----VRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPLTLC 53
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CURRENT APPLICATION NUMBER: US/09/764,874
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-08
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-28
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                 PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,215
PRIOR APPLICATION NUMBER: 60/249,214
PRIOR PELING DATE: 2000-11-17
PRIOR PELING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-16
PRIOR PELING DATE: 2000-09-08
PRIOR PELING DATE: 2000-09-14
PRIOR PELING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,221
PRIOR APPLICATION NUMBER: 60/241,221
PRIOR PELING DATE: 2000-10-20
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APPLICATION NUMBER: 60/233,065
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APPLICATION NUMBER: 60/249,211
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Matches 18; Conservative
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PRIOR APPLICATION NUMBER: 60/236,368
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/251,868
PRIOR APPLICATION NUMBER: 60/259,344
PRIOR FILING DATE: 2000-12-08
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/239,344
PRIOR FILING DATE: 2000-09-01 NR APPLICATION NUMBER: 60/220,963

R FILING DATE: 2000-07-26

R APPLICATION NUMBER: 60/217,496

R FILING DATE: 2000-07-11

R APPLICATION NUMBER: 60/225,447

R FILING DATE: 2000-08-14

R APPLICATION NUMBER: 60/218,290

R APPLICATION NUMBER: 60/218,290

R APPLICATION NUMBER: 60/218,797

R FILING DATE: 2000-07-14

R FILING DATE: 2000-08-14 DR APPLICATION NUMBER: 60/216,880

DR FILING DATE: 2000-07-07

DR APPLICATION NUMBER: 60/225,270

DR APPLICATION NUMBER: 60/25,270

DR APPLICATION NUMBER: 60/251,869

DR APPLICATION NUMBER: 60/251,869

DR APPLICATION NUMBER: 60/235,834

DR FILING DATE: 2000-09-27

DR APPLICATION NUMBER: 60/234,223

DR FILING DATE: 2000-09-21

DR APPLICATION NUMBER: 60/234,233

R FILING DATE: 2000-09-21

DR APPLICATION NUMBER: 60/224,518

DR FILING DATE: 2000-09-14

DR APPLICATION NUMBER: 60/224,518

DR FILING DATE: 2000-09-29

DR APPLICATION NUMBER: 60/224,518

DR FILING DATE: 2000-09-29

DR APPLICATION NUMBER: 60/224,519

DR APPLICATION NUMBER: 60/220,964 R FILING DATE: 2000-10-20
R APPLICATION NUMBER: 60/244,617
R FILING DATE: 2000-11-01
R APPLICATION NUMBER: 60/225,268
R FILING DATE: 2000-08-14
R APPLICATION NUMBER: 60/336,368 APPLICATION NUMBER: 60/225,758 FILING DATE: 2000-08-14 APPLICATION NUMBER: 60/216,647 FILING DATE: 2000-07-07 APPLICATION NUMBER: 60/225,267 FILING DATE: 2000-08-14 APPLICATION NUMBER: 60/241,809
APPLICATION NUMBER: 60/241,809
TITME DATE: 2000-10-20 FILING DATE: 2000-09-01
APPLICATION NUMBER: 60/229,513
FILING DATE: 2000-09-05
APPLICATION NUMBER: 60/231,413
FILING DATE: 2000-09-08 APPLICATION NUMBER: 60/226,868 FILING DATE: 2000-08-22 APPLICATION NUMBER: 60/249,299 FILING DATE: 2000-11-17 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/236,327 FILING DATE: 2000-09-29 APPLICATION NUMBER: 60/241,785 FILING DATE: 2000-09-25 APPLICATION NUMBER: 60/229,343 APPLICATION NUMBER: 60/229,345 FILING DATE: 2000-09-01
APPLICATION NUMBER: 60/229,287 FILING DATE: 2000-09-01 PRIOR
PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR

PRIOR APPLICATION NUMBER: 60/236, 367
PRIOR FILING DATE: 2000-09-05
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/236, 367
PRIOR FILING DATE: 2000-10-02
PRIOR PELICATION NUMBER: 60/237, 039
PRIOR PELICATION NUMBER: 60/237, 039
PRIOR PELICATION NUMBER: 60/237, 039
PRIOR APPLICATION NUMBER: 60/237, 030
PRIOR APPLICATION NUMBER: 60/237, 040
PRIOR APPLICATION NUMBER: 60/237, 040
PRIOR PELING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/237, 040
PRIOR PELING DATE: 2000-10-02
PRIOR PELING DATE: 2000-10-02
PRIOR PELING DATE: 2000-10-02
PRIOR PELING DATE: 2000-10-13
PRIOR PELING DATE: 2000-11-17
PRIOR PELING DATE: 2000-11-

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37.5%; Pred. No. -
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PRIOR FILING DATE: 2001-03-16
PRIOR PLILING DATE: 2001-03-16
PRIOR FILING DATE: 1998-09-08
PRIOR PLILING DATE: 1998-03-06
PRIOR PLILING DATE: 1998-03-06
PRIOR FILING DATE: 1997-03-07
PRIOR PLILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,333
PRIOR APPLICATION NUMBER: 60/040,333
PRIOR APPLICATION NUMBER: 60/040,333
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,633
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APPLICATION UNMBER: 60/047,598
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,613
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APPLICATION NUMBER: 60/047,583
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,617
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APPLICATION UNMBER: 60/047,618
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,503
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APPLICATION NUMBER: 60/047,584
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/040,334
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APPLICATION NUMBER: 60/040,336
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APPLICATION NUMBER: 60/040,163
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/047,600
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APPLICATION NUMBER: 60/047,597
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APPLICATION NUMBER: 60/047,592
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APPLICATION NUMBER: 60/047,581
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APPLICATION NUMBER: 60/047,587
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                                                                                                                                                                                         ; Sequence 362, Application US/09882171; GENERAL INFORMATION:
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                       21; Conservative
       Best Local Similarity
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                         Matches
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GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REPERENCE: P2002P2
CURRENT APPLICATION NUMBER: US/09/809,391
CURRENT FILING DATE: 2001-03-16
FILO APPLICATION date removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 761
SOFTWARE: PatentIn Ver. 2.0
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25.8%; Score 73; DB 21; Length 85;
Best Local Similarity 30.5%; Pred. No. 0.67;
Matches 18; Conservative 11; Mismatches 16; Indels
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R FILING DATE: 2000-09-08

R FILING DATE: 2000-09-08

R APPLICATION NUMBER: 60/233,064

R FILING DATE: 2000-09-14

R FILING DATE: 2000-09-14

R FILING DATE: 2000-09-14

R FILING DATE: 2000-09-14

R APPLICATION NUMBER: 60/233,063
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R FLING DATE: 2000-10-20
R APPLICATION NUMBER: 60/246,475
R FILING DATE: 2000-11-08
R FILING DATE: 2000-13-08
R FILING DATE: 2000-09-08
R PILICATION NUMBER: 60/231,243
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R RAPELICATION NUMBER: 60/241,808
R REILING DATE: 2000-10-20
R APPLICATION NUMBER: 60/241,826
R FILING DATE: 2000-10-20
R PILING DATE: 2000-10-20
R PILING DATE: 2000-10-20
                                                                                               R APPLICATION NUMBER: 60/231,242
R FILING DATE: 2000-09-08
R APPLICATION NUMBER: 60/231,414
       FILING DATE: 2000-11-17
APPLICATION WUMBER: 60/249,297
FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/232,400
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APPLICATION NUMBER: 60/232,399
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APPLICATION NUMBER: 60/232,401
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                                                                               FILING DATE: 2000-09-14
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TYPE: PRT
ORGANISM: Homo sapiens
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LOCATION: (132)
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22.8%; Score 64.5; DB 22; Length 132;

Query Match

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17; Gaps
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                                                                         9; Indels
                                                                                                                                                                                                                                                           APPLICANT: Ruben et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P2
CURRENT APPLICATION NUMBER: US/09/882,171
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 09/809,391
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PRIOR FILING DATE: 1997-66-06
PRIOR PELING DATE: 1997-66-06
PRIOR APPLICATION NUMBER: 60/056,886
PRIOR PILING DATE: 1997-08-22
PRIOR PILING DATE: 1997-08-22
PRIOR PILING DATE: 1997-08-22
PRIOR PILING DATE: 1997-08-22
PRIOR PLING DATE: 1997-08-22
PRIOR PLING DATE: 1997-08-22
PRIOR PELING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,893
PRIOR PILING DATE: 1997-08-22
PRIOR PELING DATE: 1997-08-22
PRIOR PELING DATE: 1997-08-22
PRIOR PELING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,872
PRIOR PELING DATE: 1997-08-22
PRIOR FILING DATE: 1997-08-22
PRIOR PELING DATE: 1997-08-22 JR FILING DATE: 1997-05-23

R APFLICATION NUMBER: 60/047,601

R FILING DATE: 1997-05-23

R FILING DATE: 1997-04-11

PRILING DATE: 1997-04-11

R PILING DATE: 1997-04-11 R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,674
R APPLICATION NUMBER: 60/043,669
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,312
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,313
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,313
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,672
R FILING DATE: 1997-04-11 R FILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,314

R APPLICATION NUMBER: 60/043,569

R FILING DATE: 1997-04-11

R PELICATION NUMBER: 60/043,569

R FILING DATE: 1997-04-11

R FILING DATE: 1997-04-11

R PILING DATE: 1997-04-11 DR FILING DATE: 1997-08-22
DR FILING DATE: 1997-08-22
DR FILING DATE: 1997-08-22
DR APPLICATION NUMBER: 60/056,888
DR FILING DATE: 1997-08-22
DR APPLICATION NUMBER: 60/056,899
DR FILING DATE: 1997-08-22
DR APPLICATION NUMBER: 60/056,894
DR FILING DATE: 1997-08-22
DR APPLICATION NUMBER: 60/056,894
DR FILING DATE: 1997-08-22
DR APPLICATION NUMBER: 60/056,911
DR FILING DATE: 1997-08-22
DR APPLICATION NUMBER: 60/056,911
DR FILING DATE: 1997-08-22
DR APPLICATION NUMBER: 60/056,914
DR FILING DATE: 1997-08-22
DR APPLICATION NUMBER: 60/056,910
DR FILING DATE: 1997-08-22 PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,612
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,632 APPLICATION NUMBER: 60/047,596 APPLICATION NUMBER: 60/043,315 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/048,974

1. 1997-08-22 NUMBER: 60/056,631 1. 1997-08-22 NUMBER: 60/056,845 1. 1997-08-22 NUMBER: 60/056,892 1. 1997-08-22 1. 1997-08-22 1. 1997-08-22 NUMBER: 60/057,761 1. 1997-08-23 NUMBER: 60/047,595 1. 1997-05-23 1. 1997-05-23	NUMBER: 60 1997-05-2 1997-05-2 1997-05-2 1997-05-2 1997-05-2 1997-05-2 1997-05-2 NUMBER: 60 1997-05-2 NUMBER: 60 1997-04-1 1997-04-1 1997-04-1 NUMBER: 60 1997-04-1 NUMBER: 60 1997-04-1 NUMBER: 60 1997-04-1 NUMBER: 60 1997-04-1 NUMBER: 60 1997-04-1 NUMBER: 60 NUMBER: 60 NUMBE	08-22 1 60/056,88 08-22 1 60/056,90 1 60/056,87 1 60/056,88 1 60/056,88 1 60/056,90 1 60/056,90 1 60/056,90 1 60/056,88 1 60/056,90 1 60/056,88 1 60/056,88 1 60/057,65 1 60
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GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc., et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA119PCT
CURRENT APPLICATION NUMBER: PCT/US01/01330
CURRENT FILING DATE: 2001-01-13
CURRENT FILING DATE: 2001-01-13
NUMBER OF SEQ ID NOS: 437
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PAll9PCT
CURRENT APPLICATION NUMBER: PCT/US01/01330
CURRENT FILING DATE: 2001-01-13
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 437
SOFTWARE: PatentIn Ver. 2.0
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                                                                                APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
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                                                                                                                                                       CURRENT FILING DATE: 2002-06-10
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US/09/149,476
PRIOR FILING DATE: 1998-09-08
PRIOR FILING DATE: 1998-09-08
PRIOR FILING DATE: 1998-09-08
NUMBER OF FILING DATE: 1998-03-06
SOFTWARE: Patentin Ver. 2.0
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; Sequence 164, Application PC/TUS0101330
; GENERAL INFORMATION:
                                         ; Sequence 362, Application US/10164861; GENERAL INFORMATION:
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13 LIVLKSFFFFKDSLTPSPRL 32
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PCT-US01-01330-218
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                        US-10-164-861-362
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RESULT 9
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Sequence 5353, Application PC/TUS0101339
Sequence 5353, Application PC/TUS0101339
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILLE REFERENCE: PC006PCT
CURRENT APPLICATION NUMBER: PCT/US01/01339
CURRENT FILING DATE: 2001-03-17
NUMBER OF SEQ ID NOS: 10231
SEQ ID NO 5353
                                                                                                                                                                                                                                                                                                                                             PCT-US01-01339-4675

Sequence 4675, Application PC/TUS0101339

GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc., et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCOOFPCT
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CURRENT FILING DATE: 2001-03-17
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4675
LENGTH: 89
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APPLICANT: Rosen et al.
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                                                                                                                                          22.6%;
60.0%;
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13 LIVLKSFFFFKDSLTPSPRL 32
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Best Local Similarity 60.07
Matches 12; Conservative
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Matches 12; Conservative
SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 218 LENGTH: 89
                                                                                                                                                                                   12; Conservative
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PCT-US01-01339-5353
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PCT-US01-01330-218
                                                                                                                                                              Best Local Similarity
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US-09-764-891-4675
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US-09-764-891-5353
; Sequence 5353, Application US/09764891
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PCOOG
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT APPLICATION NUMBER: US/09/764,891
; FILE REFERENCE: PCOOG
; CURRENT APPLICATION NUMBER: US/09/764,891
; FILE REFERENCE: POST: 2.0
; SEQ ID NOS: 10231
; SEQ ID NO 5353
; LENGTH: 89
; LENGTH: 89
; TYPE: PRT

ORGANISM: Homo sapiens
US-09-764-891-5353
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; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies; FILE REFERENCE: PCO06
CURRENT APPLICATION NUCLE: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper, NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4675
LENGTH: 89
TYPE: PRT
TYPE: PRT
CORGANISM: Homo sapiens
US-09-764-891-4675
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November 21, 2002, 13:41:56; Search time 10 Seconds (without alignments) 186.011 Million cell updates/sec
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1 MRRCVRHVLGIGLIVLKNLY......FOEAFLFFFLILKNPLTLCS
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1: /cgn2_6/ptodata/1/paa/VECT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

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3: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum Match 1008
                                                                                                                                                                                                                                                                     US-09-776-724A-142
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Database :

	Description	Sequence 4480, Ap	1435,	Sequence 69043, A	190.	512,	512,	512,	512,		512,	512,	512,	512,	512,		512,		512,		512,	512,	512,	512,	512,	512,	512,
SUMMARIES	ID	-10-092	-264	-09-724-676-69	-10 - 230 - 437 - 1	-10-131-813A	31-819A-5	-10-131-823A-51	-10 - 131	-10-131-	-10-131-829A-	0-125	-10 - 127	-10 - 127	-10 - 127	0 - 127	-10 - 127	-10 - 127	-10 - 127	-10 - 128	-10-131	-10-131	10 - 131 -	-10-125	7	-10-127-838B-	US-10-127-843A-512
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Sequence 1435, Application US/10264237
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PAI31P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2000-05-19

US-10-264-237-1435

RESULT 2

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RESULT Seque Seque Constitution Result Resul	SULT 1 -10-092-411A-4480 Sequence 4480, Application US/10 GENERAL INFORMATION: APPLICANT: Lynn Doucette-Stamm TITLE OF INVENTION: EPIDERMID FILE REFERENCE: 032796-101 CURRENT APPLICATION NUMBER: US, CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US of PRIOR FILING DATE: 1998-08-13 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 NUMBER OF SEQ ID NOS: 5676 LENGTH: 673 TYPE: PRI	2-411A-4480 2c 4480, Applicate Abolicate Abolicate Abolication Corresponding About Abolication Application Applica	lication US/1005 N: Oucette-Stamm et Oucette-Stamm et N: NUCLEIC ACID N: EPIDERMIDIS 32796-101 ON: NUMBER: US/10 NUMBER: US 09/1 1998-08-13 1997-11-08 NUMBER: US 60/C 1997-11-08 NUMBER: US 60/C 1997-11-08 NUMBER: US 60/C	US/ Stam Stam St. U 1-13 US US US	10-092-411A-4480 10-092-411A-4480 ENDERAL INFORMATION: APPLICANT: Lynn Doucette-Stamm et al APPLICANT: Lynn Doucette-Stamm et al APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: DATE: D32796-101 CURRENT PEPLICATION NUMBER: US/10/092,411A PRIOR FILING DATE: 1998-08-13 PRIOR FILING DATE: 1998-08-13 PRIOR FILING DATE: 1998-08-13 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-08-14 NUMBER OF SEQ ID NOS: 5676 LENGTH: 673 TYPE: PRI	TING TO	STAPHYLOCOCC
; US-10 Que Bes Mat	OKGANISM: S' -10-092-411A Query Match Best Local Sin Matches 20;	: Staphylococcus 1A-4480 h 20 Similarity 32 20; Conservative	coccus epi 20.7%; 32.3%; vative	epi 78; 38;	.dermidis Score 58.5; DB 6; Length 673 Pred. No. 3.1; 7; Mismatches 14; Indels	; 21; Gaps	
oy Oy	6 RHVL- :: 21 RHIIV 47 KN 48 79 AN 80	/PFISVISI	GIGLIVLK : LFGIEYILLS	IVE ILL	RHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLIL ::	FFLIL 46 FLIY 78	

Thu Nov 21 16:07:41 2002

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US-10-131-813A-512
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                                                                                                                                                                                                                            ; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids US-10-264-237-1435
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APPLICANT: Goddard, Paul J.
APPLICANT: Gramaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Collin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/10/230,437
CURRENT APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/069313
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
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                                                                                                                                                                                                                                                                                                     19.6%; Score 55.5; DB 6; Length 172; 31.1%; Pred. No. 2; tive 13; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                           74 VLGLWMVNVVFSFGHRLLNFQSARVTYFVNASLFIYLV-HHPLTL 117
                                                                                                                                                                                                                                                                                                                                                                                                             8 VLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPLTL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 69043, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 69043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MRRCVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEA 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 190, Application US/10230437 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 31.1%
Matches 14; Conservative
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NUMBER OF SEQ ID NOS: 2876
SOFTWARE: Patentin Ver. 3.1
                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                 NAME/KEY: MISC_FEATURE
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US-10-230-437-190
                                                SEQ ID NO 1435
LENGTH: 172
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                                                                                                      TYPE: PRT
                                                                                                                                                                                                         LOCATION:
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PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-12-17
PRIOR PLICATION NUMBER: 60/069873
PRIOR PLICATION NUMBER: 60/079294
PRIOR PLICATION NUMBER: 60/079294
PRIOR PLICATION NUMBER: 60/079294
PRIOR PLICATION NUMBER: 60/079265
PRIOR PAPLICATION NUMBER: 60/079656
PRIOR PLING DATE: 1998-03-25
PRIOR PLING DATE: 1998-03-26
PRIOR PLING DATE: 1998-03-26
PRIOR PLING DATE: 1998-03-27
PRIOR PLING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
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PRIOR PLING DATE: 1998-03-26
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C139
CURRENT APPLICATION NUMBER: US/10/131,813A
CURRENT PILING DATE: 2002-04-24
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32.5%; Pred. No. 24;
tive 10; Mismatches 17; Indels
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PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR PELICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-09-26
PRIOR PELICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/059263
FILING DATE: 1997-09-18
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APPLICATION NUMBER: 60/059122
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APPLICATION NUMBER: 60/059184
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Matches 13; Conservative
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Gurney, Austin L.
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Filvaroff, Ellen
Gao, Wei-Qiang
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ORGANISM: Homo Sapien
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Gaps

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17; Indels

DB 6; Length 716;

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11 IGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPL 50
                                                            Query Match
18.4%; Score 52; DB (Best Local Similarity 32.5%; Pred. No. 24; Matches 13; Conservative 10; Mismatches
             US-10-131-819A-512
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C134
CURRENT APPLICATION NUMBER: US/10/131,819A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/049911
                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                     PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
REmaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
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                                                                                                                                                                                                                                                                                                     Query Match 18.4%; Score 52; DB 6; Length 716; Best Local Similarity 32.5%; Pred. No. 24; Matches 13; Conservative 10; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   11 IGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPL 50
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PRIOR PELING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
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PRIOR PELING DATE: 1997-09-18
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PRIOR PELING DATE: 1997-09-18
PRIOR PELING DATE: 1997-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 512, Application US/10131819A GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: 60/059352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gerritsen, Mary E.
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Wood, William
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumas, Daniel
                                                                                                                                                                                                                           ; ORGANISM: Homo Sapien
US-10-131-813A-512
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ORGANISM: Homo Sapien
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                                                                                                                                                   SEQ ID NO 512
LENGTH: 716
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LENGTH: 716
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CURRENT APPLICATION NUMBER: 05/049911

PRIOR PAPLICATION NUMBER: 05/049911

PRIOR PAPLICATION NUMBER: 05/049911

PRIOR PAPLICATION NUMBER: 05/05914

PRIOR PAPLICATION NUMBER: 05/05914

PRIOR PAPLICATION NUMBER: 05/05913

PRIOR PAPLICATION NUMBER: 05/05913

PRIOR PAPLICATION NUMBER: 05/059113

PRIOR PAPLICATION NUMBER: 05/059115

PRIOR PAPLICATION NUMBER: 05/059115

PRIOR PAPLICATION NUMBER: 05/059115

PRIOR PAPLICATION NUMBER: 05/059117

PRIOR APPLICATION NUMBER: 05/05912

PRIOR APPLICATION NUMBER: 05/05912

PRIOR PAPLICATION NUMBER: 05/05912

PRIOR PAPLICATION NUMBER: 05/05912

PRIOR PAPLICATION NUMBER: 05/05913

PRIOR PAPLICATION NUMBER: 05/05913

PRIOR PAPLICATION NUMBER: 05/05935

PRIOR PAILING DATE: 1997-09-19

PRIOR PILING DATE: 1997-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zenin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C143
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                        Sequence 512, Application US/10131823A
                                                                                                                                                                                                                                                                                                                                                                                                                                        Stewart, Timothy A.
                                                                                                                                                                                                                                                            Gerritsen, Mary E
                                                                                                               Beresini, Maureen
                                                                                                                                                                                                                                                                                                                   Godowski, Paul J.
Gurney, Austin L.
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                                                                                                                                                                                                                                                                                                                                                                               Sherwood, Steven
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Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       Smith, Victoria
                                                                                                                                                                                                                                                                                          Goddard, Audrey
                                                                                    APPLICANT: Baker, Kevin P.
                                                                                                                                                DeForge, Laura
                                                                                                                                                                           Desnoyers, Luc
                                                                                                                                                                                                                                 Gao, Wei-Qiang
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                                                   GENERAL INFORMATION:
US-10-131-823A-512
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LENGTH: 716
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APPLICANT: Stewart/Indicty A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
APPLICANT: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C126
CURRENT APPLICATION NUMBER: US/10/131,824A
CURRENT FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/05974
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 VGLDSLESLSFYDNKLVKVPQLALQKVPNLKFLDLNKNPI 275
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APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
                                              Sequence 512, Application US/10131824A GENERAL INFORMATION:
                                                                                                                                                                                                                                                  Gerritsen, Mary E.
                                                                                                APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maureen
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Best Local Similarity 32.58
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                 Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                   Sherwood, Steven
Smith, Victoria
                                                                                                                                                                            Desnoyers, Luc
Filvaroff, Ellen
                                                                                                                                                                                                                                                                          Goddard, Audrey
                                                                                                                                                                                                                           Gao, Wei-Qiang
                                                                                                                                                    DeForge, Laura
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CORGANISM: Homo Sapien
US-10-131-824A-512
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US-10-131-826A-512
RESULT 8
US-10-131-824A-512
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APPLICANT: watanabe,Colin K
APPLICANT: watanabe,Colin K
APPLICANT: Wood,William
APPLICANT: Abod,William
APPLICANT: Shady, Zehin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE REPERBNE: P3330RIG1128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRICA PAPLICATION NUMBER: 60/049911
PRICA PAPLICATION NUMBER: 60/049911
PRICA PAPLICATION NUMBER: 60/049911
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PRIOR FILING DAME: 1997-08-26
PRIOR PELICATION NUMBER: 00/059113
PRIOR APPLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/059115
PRIOR PILING DATE: 1997-09-17
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PRIOR FILING DATE: 1997-09-17
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PRIOR FILING DATE: 1997-09-19
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
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Stewart, Timothy A.
                                                                                                                                                                      Stewart, Timothy A. Tumas, Daniel
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Gerritsen, Mary E.
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Gurney, Austin L.
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Best Local Similarity 32.5%
Matches 13; Conservative
                                Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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                                                                                                                                                  Smith, Victoria
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ORGANISM: Homo Sapien
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LENGTH: 716
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Smith, Victoria
Stewart, Timothy A.
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Wood, William
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Filvaroff, Ellen
Gao, Wei-Qiang
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ORGANISM: Homo Sapien
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LENGIH: 716
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PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059127
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR PILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR PILING DATE: 1997-09-19
                                         APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P33330R1C138
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CURRENT APPLICATION NUMBER: US/10/125,926A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/049911
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PRIOR APPLICATION NUMBER: 60/059115
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PRIOR APPLICATION NUMBER: 60/056974
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Wood, William
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APPLICANT: Beresini, Maureen
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Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
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Smith, Victoria
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Wood, William
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LENGTH: 716
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FRIOR APPLICATION NUMBER 06 059113
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11 IGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPL 50
                          ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-127-831A-512
  LENGTH: 716
                                                                                                                                 Query Match
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C107
CURRENT APPLICATION NUMBER: US/10/127,831A
CURRENT FILING DATE: 2002-10-15
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                     PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR PLICATION NUMBER: 60/059352
PRIOR PLICATION NUMBER: 60/059588
PRIOR PLICATION NUMBER: 60/059588
PRIOR PLICATION DATE: 1997-09-19
PRIOR PLICATION DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
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Best Local Similarity 32.5%; Pred. No. 24;
Matches 13; Conservative 10; Mismatches
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PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
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PRIOR PLING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/059115
PRIOR PLING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059127
PRIOR APPLICATION NUMBER: 60/059184
PRIOR APPLICATION NUMBER: 60/059184
PRIOR PILING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
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PRIOR FILING DATE: 1997-09-17
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Gurney, Austin L.
Sherwood, Steven
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Watanabe, Colin K
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Filvaroff, Ellen
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SEQ ID NO 512
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US-10-127-829A-512
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LENGTH: 716
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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DB 6; Length 716; 24;
  18.4%; Score 52; DB 6; Length 716
32.5%; Pred. No. 24;
tive 10; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/127,835A CURRENT FILING DAFE: 2002-10-15 PRIOR APPLICATION NUMBER: 60/049911 PRIOR FILING DATE: 1997-06-18
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PRIOR FILING DATE: 1997 00-16
PRIOR PELING DATE: 1997 00-16
PRIOR APPLICATION NUMBER: 60/059113
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PAPLICATION NUMBER: 60/059115
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR PELING DATE: 1997-09-18
PRIOR PELING DATE: 1997-09-18
PRIOR PELING DATE: 1997-09-18
PRIOR PELING DATE: 1997-09-18
PRIOR PELING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059589
PRIOR PELING DATE: 1997-09-19
PRIOR PELING DATE: 1997-09-19
PRIOR PELING DATE: 1997-09-19
                                                                                                                                                                                                                                                                                 Sequence 512, Application US/10127835A GENERAL INFORMATION:
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Filvaroff, Ellen
Gao, Wei-Qiang
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Wood, William
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                            Best Local Similarity 32.5%
Matches 13; Conservative
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-127-835A-512
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LENGTH: 716
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3330R1C96
CURRENT APPLICATION NUMBER: US/10/127,837A
CURRENT FILING DATE: 1997-06-18
PRIOR PELICATION NUMBER: 60/049911
PRIOR APPLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/059115
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-19
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236 VGLDSLESLSFYDNKLVKVPQLALQKVPNLKFLDLNKNPI 275
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                                                                                                                 US-10-127-837A-512; Sequence 512, Application US/10127837A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                              Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Smith, Victoria
Stewart, Timothy A.
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Watanabe, Colin K
Wood, William
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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18.4%
Best Local Similarity 32.5%
Matches 13; Conservative
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Filvaroff, Ellen
Gao, Wei-Qiang
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CORGANISM: Homo Sapien
US-10-127-837A-512
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LENGTH: 716
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OM protein - protein search, using sw model

November 21, 2002, 13:40:48; Search time 18 Seconds (without alignments) 288.403 Million cell updates/sec Run on:

1 MERCVRHVLGIGLIVLKNLY......FQEAFLFFFLILKNPLTLCS 54 US-09-776-724A-142 Perfect score; Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08 Maximum Match 1008 Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

2000	hypothetical prote probable membrane mannosyltransferas hypothetical protein protein kinase Xa2 protein coupled protein glutamine ABC transpressing protein glutamine ABC transpressing protein p
SUMMARIES	T09895 S64364 E61142 T32214 T10727 AD0114 AD0114 C49897 T28263 T28263 T28263 T28263 T28634 A6347 AC1185 AB1543 AC1185 AB1543 T26464 AC1185 AB1543 T26464 T26464 T26464 T26464 T26464 T26464 T14435 T26464 T26464 T26464 T14435 T2666 T2666 T14435 T2666 T14435 T2666 T14435
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Score	82 82 82 82 82 82 82 82 82 82 82 82 82 8
Result No.	1 1 2 2 4 3 2 7 4 4 3 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

A:Gene: MIPS:YGR069w
A:Cross-references: SGD:S0003301
A:Map position: 7R
C:Superfamily: Saccharomyces probable membrane protein YGR069w
C:Keywords: transmembrane #status predicted <TWM>F:31-47/Domain: transmembrane #status

21.2%; Score 60; DB 2; Length 111;

Query Match

penicillin-binding probable membrane ribonucleoside-dip tRNA splicing endo hypothetical prote hypothetical prote hypothetical prote mcs2 protein major core protein major core protein major core protein major core protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical 191.1
588 2 B71802 588 2 E64715 633 2 S49788 194 2 T40065 397 2 C84078 2971 2 T08026 230 2 S09778 322 2 S3580 386 2 T09709 644 1 FOVZZW 644 2 T97390 784 2 C90089 784 2 C90089
54 19.1 54 19.1 54 19.1 54 19.1 54 19.1 53.5 18.9 53.5 18.9 53 18.7 53 18.7
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

ALIGNMENTS

RESULT 1 709895 hypothetical protein T22A6 C;Species: Arabidopsis tha C;Date: 16-Jul-1999 #seque C;Accession: T09895 R;Bevan, M; Zimmermann, W submitted to the Protein S A;Reference number: Z16896 A;Accession: T09895 A;Accession: T09895 A;Accession: T09895 A;Residues: 1-395 <bev> A;Residues: 1-395 <bev> A;Cross-references: EMBL:AI A;Experimental source: cult C;Genetics: A;Gene ATES:T22A6.150 A;Map position: 4 C;Superfamily: Arabidopsis</bev></bev>	RESULT 1 109895 Hypothetical protein T22A6.150 - Arabidopsis thaliana C.Species: Arabidopsis thaliana (mouse-ear cress) C.Species: A.Steremann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; A.Steference number: Z16896 A.Scession: T09895 A.Scession: T09895 A.Scession: T09895 A.Stoos-references: EMEL:AL078637; GSPDB:GN00062; ATSP:T22A6.150 C.Genetics: C.Genetics: C.Genetics: A.Step position: 4 A.Nab position: 4 C.Superfamily: Arabidopsis thaliana hypothetical control of the cont
Query Match Best Local Sim Matches 17; Qy 4 CVRHVL Db 294 CLGEFL	Query Match 22.3%; Score 63; DB 2; Length 395; Best Local Similarity 33.3%; Pred. No. 2.4; Matches 17; Conservative 8; Mismatches 22; Indels 4; Gaps 1; 4 CVRHVLGIGLIVLENLYPHENSYMYPSPKLSSFQBAFLFFFLILKNPL 50
RESULT 2 S64364 Probable membrane N;Alternate names C;Species: Sacche C;Date: 17-May-1; C;Accession: S643 R;Wedler, H.; Sch submitted to the	RESULT 2 S64364 Probable membrane protein YGR069w - yeast (Saccharomyces cerevisiae) NiAlternate names: hypothetical protein 64554 C;Species: Saccharomyces cerevisiae C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 19-Apr-2002 R;Wedler, H.; Schafe, M.; Wedler, E.; Wambutt, R. submitted to the Protein Sequence Database, May 1996
A Accession: S64364 A Accession: S64364 A Molecule type: DNA A Residues: 1-111 (WED> A Experimental source: EMB A Experimental source: A EMB A CANN A	356 L:272853; NID:91323091; P strain S288C

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Best Local Similarity 30.49
Matches 17; Conservative
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A; Residues: 1-153 <VOE>
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Matches 18; Conserv
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                                                                                                                                                                                                                           mannosyltransferase - Methanobacterium thermoautotrophicum (strain Delta H)

C:Species: Methanobacterium thermoautotrophicum
C:Dspecies: Methanobacterium thermoautotrophicum
C:Dspecies: Methanobacterium thermoautotrophicum
C:Dspecies: Methanobacterium thermoautotrophicum
C:Date: 05-Dec.1997 #sequence_revision 05-Dec.1997 #text_change 24-Nov-1999
C;Accession: E69142
R:Smith. D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
R:Smith. D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Rismith. D.R.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: GB:AE000818; GB:AE000666; NID:G2621384; PIDN:AAB84837.1; PID:g262138
A,Experimental source: strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Start codon: GTG
C;Superfamily: Methanobacterium thermoautotrophicum dolichyl-phosphate mannose synthase
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C;Species: Caenorhabditis elegans
C;Species: 29-0ct-1999 #sequence_revision 29-0ct-1999 #text_change 29-0ct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.2%; Score 60; DB 2; Length 221; 30.9%; Pred. No. 3.2; tive 8; Mismatches 15; Indels
                     20; Indels
                                                                   4 CVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPL 50
                                                                                                    C, Accession: T32214
R; Murray, J: Wohldmann, P.; Bauer, C.; Biewald, T.
R; Murray, J: Wohldmann, P.; Bauer, C.; Biewald, T.
Submitted to the EMBL Data Library, September 1997
A; Description: The sequence of C. elegans cosmid T03D3.
A; Reference number: Z21136
A; Accession: T32214
A; Status: preliminary; translated from GB/EMBL/DDBJ
Best Local Similarity 34.0%; Pred. No. 1.5;
Matches 16; Conservative 5; Mismatches
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A; Introns: 109/3; 235/3; 269/3; 326/2
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A; Residues: 1-394 <MUR>
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A; Residues: 1-221 <MTH>
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C. Davies very Month and M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Date: 17-May 1996 #sequence_revision 17-May-1996 #text_change 19-Apr-2002 C.Date: 17-May 1996 #sequence_revision 17-May 1996 #text_change 19-Apr-2002 C.Date: 17-May 1996 #sequence_revision 17-May 1996 #sequence_revision 17-May 1996 #text_change 19-Apr-2002 C.Date: 17-May 19-Apr-2002 C.Date: 17-May
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA,
A; Residues: 1-612 <SON>
A; Cross-treferences: EMBL: U72726; NID: 92586078; PIDN: AAB82753.1; PID: 92586081
A; Experimental source: strain IRBB21
protein kinase Xa21 (EC 2.7.1.-) D, receptor type - long-staminate rice (Species: Oryza longistaminata (long-staminate rice) (S.Species: Oryza longistaminata (long-staminate rice) (C.Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000 (S.Accession: T10727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18; Indels 13; Gaps
                                                                                                                                                                                                                                        R; Song, W.Y.; Pi, L.Y.; Wang, G.L.; Gardner, J.; Holsten, T.; Ronald, P.C. plant Cell 9, 1279-1287, 1997 Arrithe: Evolution of the rice xa21 disease resistance gene family. A; Reference number: 215276; MUID:97432142; PMID:9286106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable membrane protein YGR293c - yeast (Saccharomyces cerevisiae) N;Alternate names: hypothetical protein G9596 C;Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.3%; Score 57.5; DB 2; Length 170; 30.4%; Pred. No. 5.1; tive 8; Mismatches 18; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.7%; Score 58.5; DB 2; Length 612; 38.3%; Pred. No. 14; tive 5; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MRRCVRHVLGIGLIVLKNLYFHKNSM---YPSP--KLSSFQEAFLFF 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Voet, M.; Volckaert, G.
submitted to the Protein Sequence Database, May 1996
A;Reference number: $64611
A;Accession: $64620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated from GB/EMBL/DDBJ
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Gaps

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Indels

Length 177;

DB 2;

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Rischweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T Genomics 23, 643-650, 1994
A; Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled recep A; Reference number: A55735; MUID:95154835; PMID:7851893
A; Secession: A55735
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-321 <WIL>
A;Cross-references: EMBL:AL110500; NID:e1542314; PIDN:CAB54485.1; CESP:Y87G2A.k
                                                                                                                  A; Accession: T28263
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-177 <AFO>
A; Cross-references: EMBL:AF063866; NID:g4049647; PIDN:AAC97649.1; PID:g4049689
C; Genetics:
A; Note: MSV102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       c; Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross_references: GB:L31580; NID:9468340; PIDN:AAA74232.1; PID:9468341 C; Superfamily: vertebrate rhodopsin C; Reywords: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.8%; Score 56; DB 2; Length 378; 32.6%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 19.8%; Score 56; DB 2; Length 321; Best Local Similarity 32.4%; Pred. No. 15;
J. Virol. 73, 533-552, 1999
A;Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A;Reference number: 220484; MUID:99102612; PMID:9847359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 CVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLIL 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein Y87G2A.k - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, September 1999
                                                                                                                                                                                                                                                                                                                                                                                                                           19.8%; Score 56; DB 36.4%; Pred. No. 8.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 KNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPL 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 NLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPL 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: clone Y87G2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Introns: 29/1; 89/1; 189/1; 299/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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A; Accession: T27463
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C;Function:
A;Description: catalyzes conversion of indoleglycerol phosphate and serine to tryptophan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Pathway: tryptophan blosynthesis
A; Note: coffactor pyridoxal phosphate; last step in pathway
A; Note: coffactor pyridoxal phosphate; last step in pathway
C; Superfamily: tryptophan synthase beta chain; tryptophan synthase beta chain; tryptophan synthase beta chain; prosphoprotein; pyridoxal phosphate
E; 4,-386/Domain: tryptophan synthase beta chain homology <TRPB>
F; 86/Shorive site: His #status predicted
F; 86/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.Munson, M.A.; Baumann, P.
J. Bacteriol. 175, 6426-6432, 1993
A.itile: Molecular cloning and nucleotide sequence of a putative trpDC(F)BA operon in A.Reference number: A49897; MUID:94012512; PMID:8407819
A.Accession: C49897
               A; Cross-references: EMBL: Z73078; NID: g1323535; PID: e243264; PID: g1323536; MIPS: YGR293c
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C;Sate: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T28263
R;Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tryptophan synthase (EC 4.2.1.20) beta chain - Buchnera aphidicola
C;Species: Buchnera aphidicola
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-399 <MUN>
A; Cross-references: EMBL: Z19055; NID: 9396655; PIDN: CAA79500.1; PID: 9396658
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 7R Saccharomyces cerevisiae probable membrane protein YGR293c C;Superfamily: Saccharomyces cerevisiae probable membrane protein C;Reywords: transmembrane protein F;6-22/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 RCVRHV---LGIGLIVLKNLYFHKNSM-----YPSPKLSSFQEAFLFFFLILKNPLT 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.0%; Score 56.5; DB 2; 27.0%; Pred. No. 6.1; iive 11; Mismatches 24;
                                                                                              R;Watson, M.D. submitted to the Protein Sequence Database, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Mismatches
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36.2%; Pred. No. 17;
                                                                                                                              A; Reference number: S64630
A, Accession: S64630
A; Molecule type: DNA
A; Residues: 1-141 < WAT>
A; Reperances: EMBL: Z73078; MIPS: YGR293c
C; Genetics:
                                                       A; Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: SGD:S0003525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 27.0%
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: C49897; S36428
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Ablogation with the protein homolog lin0882 [imported] - Listeria innocua (strain Clip11 C; Species: Listeria innocua C; Species: Listeria in Species: Listeria Species: C; Macuero, F.; Berche, P.; Bloec C; Dones, D.; Dominguez-Bernal, G; Duchaud, E.; Durand, A.; Baquero, F.; Berche, P.; Bloec D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A; Authors: Karst, U.
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kunn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla A; Reference number: AB1077; MUD:21537279; PMID:11679669
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Status: DNA
A; Status: L1494 <cInst Ab1543
A; Cross-references: GB:AL592022; PIDN:CAC96114.1; PID:g16413332; GSPDB:GN00178
C; Genetics:
A; Genetics
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1185
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                             A; Residues: 1-491 <GLA>
A; Cross-references: GB:NC_003210; PIDN:CAC98961.1; PID:916410286; GSPDB:GN00177
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19.8%; Score 56; DB 2; Length 491;
Best Local Similarity 28.6%; Pred. No. 24;
Matches 12; Conservative 9; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 56; DB 2; Length 494;
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                                                                                                                                                                                                                                                                                                                                                                                                                   A) Experimental Source: strain EGD-e C; Genetics: A; Genetics: A; Gene: lmo0883 C; Superfamily: Bacillus subtilis hypothetical protein ydbT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 GIRIKYGLIFRKNIYIPYERIQIVQKKQWFFFI----PFNVC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 GLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPLTLC 53
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Job time : 20 secs
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Best Local Similarity 28.69
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                                                                                                                                                                      Dranched-chain alpha keto-acid dehydrogenase EI alpha chain [imported] - Arabidopsis that C. Species: Arabidopsis thaliana (mouse-ear cress)
C. Species: Arabidopsis thaliana (mouse-ear cress)
C. Accession: T51858
C. Acc
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R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin. C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000

A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A.Reference number: A86141; MUID:21016719; PMID:11130712
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A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 1
C;Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-bin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  branched-chain alpha keto-acid dehydrogenase E1-alpha subunit [imported] - Arabidopsis
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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A;Molecule type: DNA
A;Residues: 1.472 <STO>
A;Cross.references: GB:AE005172; NID:g9454571; PIDN:AAF87894.1; GSPDB:GN00141
C;Genetics:
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AC1185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
19.8%; Score 30; Du., Matches 16; Conservative 10; Mismatches 19; Indels
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Best Local Similarity 34.08
                                                                                           RESULT 12
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GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on:

November 21, 2002, 13:42:31; Search time 10 Seconds

(without alignments)

84.572 Million cell updates/sec

105-09-776-724A-142

Perfect score: 283
Sequence: 18LOSUM62
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 100480 seqs, 15661496 residues

Total number of hits satisfying chosen parameters: 100480
Maximum DB seq length: 0
Maximum Match 0%
Maximum Maximum Match 0%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 35, Appl Sequence 36, Appl Sequence 58, Appl Sequence 38, Appl Sequence 67, Appl Sequence 67, Appl Sequence 130, Appl Sequence 130, Appl Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 64, Appli Sequence 64, Appli Sequence 64, Appli Sequence 64, Appli Sequence 64, Appli Sequence 64, Appli Sequence 15, Appli Sequence 15, Appli Sequence 7, Appli
SUMMARIES	ID	US-09-761-288-35 US-09-761-288-36 US-09-761-288-4 US-09-761-288-4 US-09-761-288-8 US-09-761-288-8 US-09-761-288-8 US-09-761-288-8 US-09-761-288-8 US-09-761-288-8 US-09-761-288-2
	DB	100 100 100 100 100 100 100 100 100
	Query Match Length DB	260 260 310 310 310 310 310 612 612 91 612 310 310 310 312 312 312 314 317 317 317 317
	Query Match	200.8 200.8
	Score	52 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
	Result No.	22 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

252 1022 1022 1022 1039 1	Sequence 180, App Sequence 44, Appl
10 US-09-801-368-252 10 US-09-815-242-4983 10 US-09-811-241-189 10 US-09-864-1020 10 US-09-764-864-1020 10 US-09-764-864-1020 10 US-09-915-242-13946 10 US-09-915-242-131 10 US-09-915-242-13 10 US-09-918-242-9 10 US-09-918-242-9 10 US-09-918-242-9 10 US-09-918-242-9 10 US-09-918-242-9 10 US-09-171-161A-269 10 US-09-771-161A-269 10 US-09-771-161A-269 10 US-09-918-2594 12 US-110-139-816-18 12 US-110-047-676A-11 12 US-110-139-816-18 12 US-110-052-586-454 10 US-09-886-055-115 10 US-09-811-132-445	0S-09-041-132-100
1993 1993 1993 1993 1993 1993 1993 1993	105 1
18.2 18.0 18.0 17.7 17.7 17.3 17.3 17.3 17.3 17.3 17.3	
0. 4 44444444 1.1111.00000.0000000000000	4.0
	4.5

ALIGNMENTS

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RESULT.

US-09-761-288-35

Sequence 35, Application US/09761288

Sequence 35, Application US/09761288

Sequence 35, Application US/09761288

Sequence 35, Application US/09761288

SEREAL INFORMATION: Muralidhara

APPLICANT: Praylag, Sudhirdan

APPLICANT: Trubier, Raymond J

APPLICANT: Trubier, Raymond J

APPLICANT: Trubier, Raymond J

APPLICANT: Li, Li,

TILLE OF INVENTION: NO. USZ0020065405Alel Polypeptides and Nucleic Acids Encoding

CURRENT FILING TOWER: S0/176,134

PRIOR APPLICATION NUMBER: 66/176,134

PRIOR APPLICATION NUMBER: 66/176,134

PRIOR PLILNG DATE: 2000-01-14

PRIOR PLILNG DATE: 2000-07-24

PRIOR PLILNG DATE: 2000-07-24

PRIOR PLILNG DATE: 2000-07-24

PRIOR PLILNG DATE: 2000-07-24

PRIOR PLILNG DATE: 2000-07-25

PRIOR PLING DATE: 2000-07-26

PRIOR PLING DATE
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TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-L TITLE OF INVENTION: LIKE) POLYPEPTIDES AND POLYNUCLECTIDES
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APPLICANT: Padigaru, Sudhirdas
APPLICANT: Padigaru, Sudhirdas
APPLICANT: Taupier, Raymond J
APPLICANT: Taupier, Raymond J
APPLICANT: Mishra, Vishnu
APPLICANT: Tchernew, Velizar
APPLICANT: Spytek, Kimberky
APPLICANT: Spytek, Kimberky
APPLICANT: 1, Li
APPLICANTON: NO. US20020065405Alel Polypeptides and Nucleic Acids Encoding
FITLE REFERENCE: 15566-638
CURRENT FILING DATE: 2001-01-16
PRIOR APPLICATION UWBER: US/09/761,288
CURRENT FILING DATE: 2001-01-16
PRIOR APPLICATION UWBER: 60/177,839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 RRCVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPL---TLCS 54
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20.8%; Score 59; DB 10; Length 304;
Best Local Similarity 30.4%; Pred. No. 1.4;
Matches 17; Conservative 9; Mismatches 24; Indels
                                                         TITLE REFERENCE: HYS-37C1P
CURRENT APPLICATION NUMBER: US/09/747,835A
CURRENT FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: US 09/729,739
PRIOR APPLICATION NUMBER: US 09/729,739
PRIOR FILING DATE: 2000-12-04
PRIOR FILING DATE: 2000-08-31
PRIOR FILING DATE: 2000-08-31
PRIOR FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: US 09/520,312
PRIOR APPLICATION NUMBER: US 09/520,317
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 63
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PATENTIN VERSION 3.0
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PRIOR APPLICATION NUMBER: 60/176,134
PRIOR FILING DATE: 2000-01.14
PRIOR FILING DATE: 2000-01.15,989
PRIOR FILING DATE: 2000-01-13
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/218,324
PRIOR PILING DATE: 2000-07-24
PRIOR PILING DATE: 2000-07-24
PRIOR FILING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: 60/178,191
PRIOR APPLICATION NUMBER: 60/178,191
PRIOR APPLICATION NUMBER: 60/178,191
PRIOR APPLICATION NUMBER: 60/178,191
PRIOR FILING DATE: 2000-01-26
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Patent No. US20020065405A1
Drmanac, Radoje T
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-747-835A-58
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LENGTH: 304
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APPLICANT: Spytek, Kimberky
APPLICANT: Li, Li
TITLE OF INVENTION: No. US20020065405Alel Polypeptides and Nucleic Acids Encoding Sam
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                                                                                                   6; Gaps
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                                                                                                                                                                        2 RRCVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPL---TLCS 54
                                                                                                                                             2 RRCVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPL---TLCS 54
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Pred. No. 1.2;
                                               20.8%; Score 59; DB 10; Length 260; 30.4%; Pred. No. 1.2;
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                                                                                                   24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 20.8%; Score 59; UB Local Similarity 30.4%; Pred. No. 1.2;
                                                                                                   9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 58, Application US/09747835A Patent No. US20020146692A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              Sequence 36, Application US/09761288 Patent No. US20020065405A1
                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
APPLICANT: Praygas, Sudhirdas
APPLICANT: Taupier, Raymond J
APPLICANT: Mishra, Vishnu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Yamazaki, Victoria APPLICANT: Tang, Y. Tom APPLICANT: Liu, Chenghua PAPPLICANT: Zhou, Ping YAPPLICANT: Wang, Dunrui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patentin Ver. 2.0
                                                      Query Match 20.8'
Best Local Similarity 30.4'
Matches 17; Conservative
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Ren, Feiyan
Asundi, Vinod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens US-09-761-288-36
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US-09-761-288-36
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LENGTH: 260
         US-09-761-288-35
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| Parent No. US20020065405A1
| GENERAL INFORMATION:
| APPLICANT: Padigaru, Muralidhara
| APPLICANT: Padigaru, Muralidhara
| APPLICANT: Taupier, Raymond J
| APPLICANT: Syytek, Kimberky
| APPLICANT: Li, Li, Li
| TITLE OF INVENTION: No. US20020065405A1el Polypeptides and Nucleic Acids Encoding
| FILE REPERENCE: 1506-638
| CURRENT APPLICATION NUMBER: 60/177,839
| PRIOR FILING DATE: 2000-01-13
| PRIOR FILING DATE: 2000-01-13
| PRIOR PAPLICATION NUMBER: 60/176,134
| PRIOR PAPLICATION NUMBER: 60/176,33
| PRIOR APPLICATION NUMBER: 60/178,191
| PRIOR PAPLICATION NUMBER: 60/178,191
| PRIOR PILING DATE: 2000-01-26
| PRIOR PAPLICATION NUMBER: 60/178,27
| PRIOR PILING DATE: 2000-01-26
| PRIOR PILING DATE: 
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                              CURRENT APPLICATION NUMBER: US/09/761,288
CURRENT PRILNG DATE: 2000-01-01-6
PRIOR PAPLICATION NUMBER: 06/17,839
PRIOR FILING DATE: 2000-01-25
PRIOR PILING DATE: 2000-01-14
PRIOR PILING DATE: 2000-01-14
PRIOR PILING DATE: 2000-01-13
PRIOR PELING DATE: 2000-01-13
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/178,191
PRIOR FILING DATE: 2000-01-26
PRIOR FILING DATE: 2000-01-26
PRIOR FILING DATE: 2000-01-26
PRIOR PRILING DATE: 2000-01-26
PRIOR PRILING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: 60/178,27
PRIOR PELLING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: 60/220,590
PRIOR APPLICATION NUMBER: 60/220,590
PRIOR APPLICATION NUMBER: 2000-07-25
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PATENTIN VET: 2.0
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APPLICANT: Toberney, Velizar
APPLICANT: Spytek, Kimberky
APPLICANT: Spytek, Kimberky
APPLICANT: Spytek, Kimberky
APPLICANT: Li
TILE REFERENCE: 15966-638
CURRENT APPLICATION NUMBER: US/09/761,288
CURRENT FILING DATE: 2001-01-16
PRIOR FILING DATE: 2000-01-25
PRIOR PRILING DATE: 2000-01-14
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-01-26
PRIOR FILING DATE: 2000-01-26
PRIOR FILING DATE: 2000-01-26
PRIOR PELICATION NUMBER: 60/218,191
PRIOR FILING DATE: 2000-01-26
PRIOR PELICATION NUMBER: 60/218,227
PRIOR PELICATION NUMBER: 60/218,227
PRIOR PELICATION NUMBER: 60/220,590
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TITLE OF INVENTION: No. US20020065405Alel Polypeptides and Nucleic Acids Encoding Sam
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                                                                                 Query Match 20.8%; Score 59; DB 10; Length 310; Best Local Similarity 30.4%; Pred. No. 1.5; Matches 17; Conservative 9; Mismatches 24; Indels
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Patent No. US20020065405A1
GENERAL INFORMATION:
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Patent No. US20020065405A1
GENERAL INFORMATION:
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APPLICANT: Prayaga, Sudhirdas
APPLICANT: Taupier, Raymond J
APPLICANT: Mishra, Vishnu
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APPLICANT: Spytek, Kimberky
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Matches 17; Conservative
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ORGANISM: Homo sapiens
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US-09-761-288-4
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Gaps

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19.6%; Score 55.5; D
38.5%; Pred. No. 1.1;
tive 7; Mismatches
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LaVallie, Edward R.
Collins-Racie, Lisa A.
Evans, Cheryl
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Patent No. US20020065394A1
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1300
LENGTH: 96
  Cafferkey, Robert
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 38.58
Matches 15; Conservative
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                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapien
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LENGTH: 91
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US-09-745-763-4
  APPLICANT:
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                                                                                                5
                                                                                                6; Gaps
                                                                                                                                                           238 RICFSHLCVIGLVYGTAIIMYVGPRYGNPK---EQKKYLLLFHSLFNPMLNPLICS 290
                                                                                                                                    2 RRCVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPL---TLCS 54
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                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Hulbert, Soct
APPLICANT: Richter, Todd
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resisitance in Plants
CORRESPONDENCE: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.7%; Score 58.5; DB 8; Length 612; 38.3%; Pred. No. 3.7;
                                                     Score 59; DB 10; Length 310;
Pred. No. 1.5;
                                                                                                24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MRRCVRHVLGIGLIVLKNLYFHKNSM---YPSP--KLSSFQEAFLFF 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,386A
FILING DATE: 13-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Finbarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                              9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        023070-058950US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 160, Application US/10001879
Patent No. US20020127237A1
GENERAL INFORMATION:
APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
                                                                                                                                                                                                                                                                       Sequence 2, Application US/08910386A Patent No. US20020092041A1 GENERAL INFORMATION:
APPLICANT: Ronald, Pamela C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02.
TELECOMMUNICATION INFORMATION:
                                                       20.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             612 amino acids
                                                                                                  Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
; ORGANISM: Homo sapiens US-09-761-288-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-001-879-160
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                                                                                                                                                                                                                                     RESULT 8
US-08-910-386A-2
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APPLICANT: Ali, Shujath
APPLICANT: Su, Yongming
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes a
FILE REFERENCE: DEX-0281
CURRENT APPLICATION NUMBER: US/10/001,879
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/252,188
PRIOR FILING DATE: 2000-11-21
SUMBER OF SEC ID NOS: 201
SOFTWARE: Patentin version 3.1
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Treacy, Maurice
Spaulding, Vikh
TITLE OF INVENTION: SECRETED PROFEINS AND POLYNUCLEOTIDES
ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 96;
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Patent No. US20020052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US/09/925,301
PRIOR PAPLICATION NUMBER: PCT/US00/05882
PRIOR APPLICATION NUMBER: 05/104,270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Thu Nov 21 16:07:40 2002

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RESULT 14
US-09-761-288-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MRRCVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPLTLCS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08910386A
Patent No. US20020092041A1
GENERAL INFORMATION:
APPLICANT: Ronald, Pamela C.
APPLICANT: Song, Wen-Yuang
APPLICANT: Hulbert, Scot
APPLICANT: Richter, Todd
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resisitance in Plants
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 18.6%; Score 52.5; DB 10; Length; Best Local Similarity 25.9%; Pred. No. 7; Matches 14; Conservative 14; Mismatches 21; Indels
                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYZHEN: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION UMBER: US/09/745,763
FILING DATE: 18-Jun -2000
CLASSIFICATION: CURROWN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSE: Twomsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                             ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (617) 498 8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 216 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: <Unknown>
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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NUMBER OF SEQUENCES: 219
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                       COUNTRY: U.S.A. ZIP: 02140
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                                                                                                               STATE: MA
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APPLICANT: TISTICAN
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APPLICANT: TOTAL AND TISTICAN
APPLICANT: TOTAL AND TISTICAN
APPLICANT: TOTAL AND TISTICAN
APPLICANT: Spytek, Kimberky
APPLICANT: Li, Li
TITLE CHEFERENCE: 15966-638
CURRENT APPLICATION NUMBER: US/09/761,288
CURRENT APPLICATION NUMBER: 60/17,839
PRIOR FILING DATE: 2000-01-15
PRIOR APPLICATION NUMBER: 60/176,134
PRIOR PILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/175,989
PRIOR FILING DATE: 2000-01-13
PRIOR APPLICATION NUMBER: 60/176,18,34
PRIOR FILING DATE: 2000-07-14
PRIOR PLING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/178,191
PRIOR PLING DATE: 2000-07-24
PRIOR FILING DATE: 2000-07-25
PRIOR PRIOR APPLICATION NUMBER: 60/178,27
PRIOR FILING DATE: 2000-01-26
PRIOR PLING PATE: 2000-01-26
PRIOR FILING DATE: 2000-01-26
PRIOR PRIOR PRIOR DATE: 2000-01-26
PRIOR FILING DATE: 2000-01-26
PRIOR PRIOR PRIOR DATE: 2000-01-26
PRIOR PRIOR PRIOR DATE: 2000-01-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                         18.6%; Score 52.5; DB 8; Length 1025; 36.2%; Pred. No. 42; tive 6; Mismatches 19; Indels 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MRRCVRHVLGIGLIVLKNLYFHKNSM---YPSP--KLSSFQEAFLFF 42
; Sequence 22, Application US/09761288
; Patent No. US20020065405A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Padigaru, Muralidhara
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Taupier, Raymond J
Mishra, Vishnu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 36.2
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 29.6
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                               US-08-910-386A-7
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LENGTH: 310
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APPLICANT:
APPLICANT:
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PRIOR APPLICATION NUMBER: 60/178,191
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CORGANISM: Homo sapiens
US-09-761-288-64
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APPLICANT: Tchernev, Velizar
APPLICANT: Tchernev, Velizar
APPLICANT: Li, Li
TTYLE OF INVENTION: US20020065405Alel Polypeptides and Nucleic Acids Encoding Sam
FILE REFERENCE: 15966-638
CURRENT FILING DATE: 2001-01-16
PRIOR PPLICATION NUMBER: 60/177,839
PRIOR PLILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 2000-01-14
PRIOR PLILING DATE: 2000-01-13
PRIOR PLICATION NUMBER: 60/175,989
PRIOR PLILING DATE: 2000-01-13
PRIOR PLILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-24
PRIOR FILING DATE: 2000-07-24
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TITLE OF INVENTION: No. US20020065405Alel Polypeptides and Nucleic Acids Encoding Sam
FILE REPRENCE: 15966-638
FILE REPRENCE: 15966-638
CURRENT APPLICATION NUMBER: US/09/761,288
CURRENT FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/176,334
PRIOR FILING DATE: 2000-01-24
PRIOR PLILING DATE: 2000-01-14
PRIOR PLILING DATE: 2000-01-14
PRIOR PLILING DATE: 2000-01-13
PRIOR PLILING DATE: 2000-01-13
PRIOR PLILING DATE: 2000-01-13
PRIOR PLILING DATE: 2000-01-13
PRIOR PLILING DATE: 2000-01-26
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PRIOR PLILING DATE: 2000-01-26
PRIOR PPLILING DATE: 2000-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 64, Application US/09761288; Patent No. US20020065405A1; GENERAL INFORMATION: APPLICANT: Padigaru, Muralidhara APPLICANT: Prayaga, Sudhirdas APPLICANT: Taupier, Raymond J. APPLICANT: Mishra, Vishnu
Sequence 24, Application US/09761288; Patent No. US20020065405A1; GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara, APPLICANT: Prayaga, Sudhirdas, APPLICANT: Taupier, Raymond J. APPLICANT: Mishra, Vishpu
                                                                                                                                                                                                                                                                                        APFLICANT: Tauples, ...
APPLICANT: Mishra, Vishnu
APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberky
IntraNT: Li, Li
Total Li

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-761-288-64
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 18.4%; Score 52; DB 10; Length 310; Best Local Similarity 29.6%; Pred. No. 12; Matches 16; Conservative 8; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: November 21, 2002, 13:46:13 Job time : 10 secs
PRIOR FILING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: 60/178,227
PRIOR FILING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: 60/220,590
PRIOR FILING DATE: 2000-07-25
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 64
LENGTH: 310
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(without alignments)
113.488 Million cell updates/sec
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283
1 MRRCVRHVLGIGLIVLKNLY......FQEAFLFFFLILKNPLTLCS
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                         OM protein
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Issued_Patents_AA:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. STIMMARTES

		dФ			SUMMARIES	
Result No.	Score	Query	Query Match Length	DB	ID	Description
н		22.8	132	4	US-09-149-476-362	Sequence 362, App
7	æ	20.7		4	-134	4480
m	26	19.8		Н	153-848-24	24. Ar
4	99	19.8		٣	9-843	24
S	56	19.8		4	-088-337B	24
9	26	19.8		Ŋ	PCT-US93-11153-24	24
7	26	19.8		m	39-299-843A	
œ	26	19.8		4	US-09-088-337B-66	99
6	S	19.8		4	US-09-108-020-12	
10	'n.	19.6		4	US-08-180-371-2	2.
11	ъ.	19.6		Ŋ	PCT-US92-05707-2	, c
12	ά.	18.6		7	US-08-475-891A-4	4
13	52.5	18.6		7	US-08-567-375-4	. 4
14	ς.	18.6	-	7	US-08-587-680A-4	4
15	52	18.4	358	Н		Sequence 19, Appl
16	52	18.4	358	m	US-09-299-843A-19	19
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20	52	18.4	361	m	-09-178-	7
21	52	18.4	378	Н	-08	7
22	52		378	-	-08-383-751A-	7
23	52		378	Н	-08-153-	15,
24	52		378	m	-08-352-678-	2,
25	52		378	m	-60-	Sequence 15, Appl
26	52	18.4	378	4	-09-251-545-	٦,
27	52	18.4	378	4	US-09-045-583-49	49,

Sequence 15, Appl Sequence 2, Appl Sequence 2, Appl Sequence 15, Appl Sequence 7, Appl Sequence 7, Appl Sequence 7, Appl Sequence 6, Appl Sequence 6, Appl Sequence 3, Appl Sequence 3, Appl Sequence 2, Appl Sequence 10, Appl Sequence 11, Appl Sequence 11, Appl Sequence 12, Appl Sequence 13, Appl Sequence 13, Appl Sequence 18, Appl Sequence 67, Appl	
378 4 US-09-088-337B-15 378 4 US-09-534-185-49 378 5 PCT-US93-09636-2 410 1 US-08-153-848-7 410 3 US-09-299-843A-7 410 4 US-09-088-337B-7 410 5 PCT-US93-11153-7 3200 2 US-08-877-451-8 415 4 US-09-088-37B-7 415 4 US-09-08-96-6 422 4 US-09-675-580-3 600 3 US-08-904-871-3 1098 3 US-08-904-871-3 1251 4 US-09-055-580-3 600 3 US-08-904-871-3 1251 4 US-09-075-580-3 1251 4 US-08-168-32-18 2523 1 US-08-185-432-18	ALIGNMENTS 476-362 8 362, Application US/09149476 No. 6240565 No. 6240565 INFORMATION: ANT: Rosen et al. DE INVENTION: APPLICATION NUMBER: US/09/149,476 I FILING DATE: 1998-09-08 R APPLICATION NUMBER: US/09/1493 R FILING DATE: 1998-03-06 R APPLICATION NUMBER: 60/040,162 R APPLICATION NUMBER: 60/040,162 R APPLICATION NUMBER: 60/040,333 R FILING DATE: 1997-03-07 R APPLICATION NUMBER: 60/040,334 R FILING DATE: 1997-03-07 R APPLICATION NUMBER: 60/040,626 R APPLICATION NUMBER: 60/040,626 R APPLICATION NUMBER: 60/040,626 R FILING DATE: 1997-03-07 R APPLICATION NUMBER: 60/040,633 R FILING DATE: 1997-03-07 R APPLICATION NUMBER: 60/040,633 R FILING DATE: 1997-03-07 R APPLICATION NUMBER: 60/047,600 R FILING DATE: 1997-05-23 R APPLICATION NUMBER: 60/047,613 R PILING DATE: 1997-05-23 R APPLICATION NUMBER: 60/047,613 R PILING DATE: 1997-05-23 R APPLICATION NUMBER: 60/047,502 R FILING DATE: 1997-05-23 R APPLICATION NUMBER: 60/047,503 R FILING DATE: 1997-05-23
52 52 52 18 52 18 52 18 52 18 52 18 52 18 54 18 54 18 55 18 56 18 57 18 58 18 59 18 50 18 50 18 50 18 50 18 50 18 50 18 50 18 50 50 50 50 50 50 50 50 50 50 50 50 50	66-36 1. 70682
22 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 US-09-149-47 Sequence 3 Patent No. GENERAL IN TITLE OF FILE OF FILE OF FILE RALIER F EARLIER F

EARLIER PELLICAIN NUMBER: 60/043, 500
EARLIER PELLING DATE: 1997-05-23
EARLIER PELLING DATE: 1997-06-23
EARLIER PELLING DATE: 1997-06-23
EARLIER PELLING DATE: 1997-06-23
EARLIER PELLING DATE: 1997-06-23
EARLIER PELLING DATE: 1997-04-11
EARLIER PELLING DATE: 1997-06-20
EARLIER PELLING DATE: 1997-0

EARLIER APPLICATION NUMBER: 60/056,894
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,636
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,910
EARLIER APPLICATION NUMBER: 60/056,910
EARLIER APPLICATION NUMBER: 60/056,910
EARLIER APPLICATION NUMBER: 60/056,845
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22 ER FILING DATE: 1997-08-22

ER FILING DATE: 1997-08-22

ER FILING DATE: 1997-08-22

ER PELING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/047,595

ER FILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/047,595

ER FILING DATE: 1997-05-23

ER APPLICATION NUMBER: 60/047,599

ER FILING DATE: 1997-05-23

ER APPLICATION NUMBER: 60/047,598

ER FILING DATE: 1997-05-23

ER FILING DATE: 1997-05-23

ER APPLICATION NUMBER: 60/047,586

ER FILING DATE: 1997-05-23

ER APPLICATION NUMBER: 60/047,590

ER FILING DATE: 1997-05-23

ER PELING DATE: 1997-05-23 R APPLICATION NUMBER: 60/043,578
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,576
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/047,501
R FILING DATE: 1997-05-23
R FILING DATE: 1997-05-23
R FILING DATE: 1997-06-23
R FILING DATE: 1997-06-23
R APPLICATION NUMBER: 60/043,670
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,632
R FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,881
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,909
APPLICATION NUMBER: 60/056,875
APPLICATION NUMBER: 60/056,875 FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,862
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,887
FILING DATE: 1997-08-22 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/057,650 FILING DATE: 1997-09-05 APPLICATION NUMBER: 60/056,884 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,876 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,908 APPLICATION NUMBER: 60/048,964 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 BARLIER F
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us-09-776-724a-142.rai

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APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 56; DB 1; Length 359;
Pred. No. 3.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: 111inois COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 CFVGLLGNGLVILTYIYFKRLKTMTDTYLLNLAVADILFLLIL 91
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
                   SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 CVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/153,848 FILING DATE: 17-NOV-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/977,452 FILING DATE: 17-NOV-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24, Application US/09299843A Patent No. 6107475 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6300
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 32.6:
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-153-848-24
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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MEDIUM TYPE: Floppy
                                                                                      FILING DATE: CLASSIFICATION:
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US-09-299-843A-24
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: 10594-04.964
PRIOR FILING DATE: 1997-11.08
PRIOR FILING DATE: 1997-11.08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
EENGTH: 673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MRRCVRH-VLGIGLIVLKNLYFHKNSMYPS-----PKLSSFQEAFL-FFFLIL 46
                                                                                                                                                                                                                                                                                         APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                   Query Match

22.8%; Score 64.5; DB 4; Length 132;
Best Local Similarity 37.5%; Pred. No. 0.057;
Matches 21; Conservative 9; Mismatches 9; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6300 Sears Tower, 233 South Wacker Drive
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
US-09-134-001C-4480
; Sequence 4480, Application US/09134001C
; Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Staphylococcus epidermidis US-09-134-001C-4480
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Godiska, Ronald
Gray, Patrick W.
Schwelkart, Vicki L.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
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                                                                                                                                                                                                                                            19.8%; Score 56; DB 3; Length 359; 32.6%; Pred. No. 3.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 6300 Sears Tower, 233 South Wacker Drive
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                                                                                                                                                                                                                                                                                     22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                               4 CVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLIL 46
                                                                                                                                                                                                                                                                                                                                                      49 CFVGLLGNGLVILTYIYFKRLKTMTDTYLLNLAVADILFLLIL 91
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APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                     7; Mismatches
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APPLICATION NUMBER: US 08/153,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: No. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24, Application US/09088337B Patent No. 6348574 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 359 amino acids
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TELECOMMUNICATION INFORMATION:
                                                                         INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
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               TELEFAX: (312) 474-6300
TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 32.6
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                     Matches 14; Conservative
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STATE: Illinois
COUNTRY: USA
                                                                                                                                                                               MOLECULE TYPE: protein
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Best Local Similarity
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                                                                                                                                                                  linear
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                                                                                                                                                                                                       US-09-299-843A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-088-337B-24
                                                                                                                                                                TOPOLOGY:
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Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
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                                                                                                                                                Sequence 24, Application PC/TUS9311153
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Schweikar, Vicki L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
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4 CVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLIL 46
                       OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US93/11153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPANNE: (312) 474-6300
TELEFAX: (312) 474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 359 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Borun
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                                                                                                                                                                                                                                                                                                                                                                                                       Chicago
Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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US-09-299-843A-66
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Gray, Patrick W.
Schweikart, Vicki L.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 19.8%; Score 56; DB 3; Length 378; Local Similarity 32.6%; Pred. No. 3.4; es 14; Conservative 7; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 CVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLIL 46
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                      PatentIn Release #1.0, Version #1.25
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APPLICATION NUMBER: US/09/088,337B
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                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/153,848 FILING DATE: 17-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 66, Application US/09088337B Patent No. 6348574 GENERAL INFORMATION:
                                                                                                                                                                  PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
                                                                                                                                               COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 66:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
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COMPUTER READABLE FORM:
                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 378 amino acids
amino acid
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Chicago
                                                                                                                                                                  OPERATING SYSTEM:
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                                         Illinois
                   Chicago
                                                             USA
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                                                                                                                                                                                        SOFTWARE:
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STREET:
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GENERAL INCORATION:
CONTRACT INCORATION:
CONTRACT MATCH TO MATCH
APPLICANT: Johnston, Mark L.
APPLICANT: Johnston, Mark L.
APPLICANT: Money, Michael H.
APPLICANT: Luethy, Michael H.
APPLICANT: Money, Brian P.
TITLE OF INVENTION: USE OF DNA ENCODING PLASTID PYRUVATE DEHYDROGENASE AND
TITLE OF INVENTION: BRANCHED CHAIN OXOACID DEHYDROGENASE COMPONENTS TO
TITLE OF INVENTION: ENHANCE POLYHYDROXYALKANOATE BIOSYNTHESIS IN PLANTS
FILE REFERENCE: UMO 1482
CURRENT APPLICATION NUMBER: US/09/108,020A
CURRENT FILING DATE: 1999-06-30
EARLIER PILING DATE: 1997-06-01
EARLIER PILING DATE: 1997-06-01
EARLIER FILING DATE: 1997-06-01
EARLIER FILING DATE: 1998-03-02
NUMBER OF SEQ ID NOS: 54

SOFTWARE: PATENTIN VEY. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.8%; Score 56; DB 4; Length 378; 32.6%; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 CFVGLLGNGLVILTYIYFKRLKTMTDTYLLNLAVADILFLLIL 111
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                                                               APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 66: US-09-088-3378-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 12, Application US/09108020A; Patent No. 6143561
; GENERAL INFORMATION:
FILING DATE: 01-Jun-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 378 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Arabidopsis thaliana US-09-108-020-12
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Best Local Similarity 34.0%
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 32.6
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
US-09-108-020-12
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RESULT 10

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STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                     APPLICANT: Choudhury, Chandra
TITLE OF INVENTION: Hematopoietic Growth Factor Derived
TITLE OF INVENTION: Hematopoietic Growth Factor Derived
TITLE OF INVENTION: 1 From T Lymphocytes and Methods of Use Therefor
WUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Darun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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GENERAL INFORMATION:
APPLICANT: Choudhury, Chandra
TITLE OF INVENTION: Hematopoietic Growth Factor Derived from
TITLE OF INVENTION: T Lymphocytes and Methods of Use Therefor NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
19.6%; Score 55.5; DB 4; Length 554;
Best Local Similarity 26.0%; Pred. No. 6.4;
Matches 13; Conservative 13; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    387 VPFQNIFWESVTESSHQTLSTFEPRLXXTFFQKHYLXFICLVTSPLSLCS 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER FRANCHEL FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/180,371
FILING DATE: 12-JAN 1994
PRIOR APPLICATION: 424
PRIOR APPLICATION NUMBER: US 906866
FILING DATE: 01 July 1992
ATTOMEY/AGENT INFORMATION:
ANAMERICATION NUMBER: OF 1000 PRIOR PRIOR PATENTAL PRIOR PATENTAL PATENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Two First National Plaza, 20 South Clark STREET: Street
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27620/31668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 6300 Sears Tower, 233 Sout CITY: Chicago STATE: 111inois COUNTRY: United States of America IP: 60606-6402
US-08-180-371-2
; Sequence 2, Application US/08180371
; Patent No. 6254861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Gruber, Lewis S.
REGISTRATION NUMBER: 30,060
REFERENCE/DOCKET NUMBER: 276
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-386
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
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MOLECULE TYPE: protein

US-08-180-371-2
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                          GENERAL INFORMATION:
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APPLICANT: Wang, Guo-Liang
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.6%; Score 55.5; DB 5; Length 554; 26.0%; Pred. No. 6.4; tive 13; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     387 VPFQNIFWFSVTESSHQTLSTFEPRLXXTFFQKHYLXFICLVTSPLSLCS 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 IVLKNLYF------HKNSMYPSPKLSS--FQEAFLFFFLILKNPLTLCS 54
                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05707
FILING DATE: 19920707
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gruber, Lewis S.
REGISTRATION NUMBER: 30,060
REFERENCE/POCKET NUMBER: 27620/30933
TELEPHONE: (312) 346-5750
TELEPA: (312) 346-5750
TELEFA: (312) 346-5760
TELERA: 25-3856
INFORMATION FOR SEO ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: U$/08/475,891A FILING DATE: 06-JUN-1995 CLASSIFICATION: 800 PRIOR APPLICATION DATA: APPLICATION NUMBER: U$ 08/373,375 FILING DATE: 17-JAN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Enhancedero Center, Eighth Floor STREET: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02370-058910US
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08475891A Patent No. 5859339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 576-0200
TELEFRAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1012 amino acids
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AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 26.09
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein PCT-US92-05707-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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Gaps
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                                                                                                                                                                                                                                    APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Mismatches 19; Indels
                                                                   1 MRRCVRHVLGIGLIVLKNLYFHKNSM---YPSP--KLSSFQEAFLFF 42
                                      1 MRRCVRHVLGIGLIVLKNLYFHKNSM---YPSP--KLSSFQEAFLFF 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/587,680A
                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 023070-058940US TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200 TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.6%; Score 52.5; DE
illarity 36.2%; Pred. No. 36;
Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION: 00.0
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-DAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/567,375
FILING DATE: 04-DEC-1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 17-JAN-1996
CLASSIFICATION: 800
NOR APPITORMENT
                                                                                                                                                                                       Sequence 4, Application US/08587680A
Patent No. 5977434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1025 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
    17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: TWO EMECACIONAL SAN Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-587-680A-4
                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 17; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-153-848-19
                                                                                                                                                                          US-08-587-680A-4
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      Matches
                                                                                                                                                        RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                         DB 2; Length 1012;
                                                              COCATION: 1.1012
OTHER INFORMATION: /note= "Xa21 Xanthomonas spp. coffer information: disease resistance polypeptide RRK-B OTHER INFORMATION: from rice (Oryza sativa)"
US-08-475-891A-4
                                                                                                                                                                                                                     Query Match 18.6%; Score 52.5; DB 2; Length 1 Best Local Similarity 36.2%; Pred. No. 36; Matches 17; Conservative 6; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                   1 MRRCVRHVLGIGLIVLKNLYFHKNSM---YPSP--KLSSFQEAFLFF 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,375 FILING DATE: 04-DEC-1995 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Bastian, Kevin L.
REGISTARTION UNDBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-058930
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-5EP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-UN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08567375 Patent No. 5952485 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.6%;
36.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-567-375-4
        TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Two Embarcac
CITY: San Francisco
STATE: California
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                                                   FEATURE:
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Sequence 19, Application US/08153848

Pater No. 7578904
GENERAL IRPORANION.
APPLICANT: Goolska, Sociald
APPLICANT: Goolska, Schoold
APPLICANT: Schweikart, Vicki L.
TTLE OF INTENTION.
ADDRESSEE: Marchall, O'Toole, Gerstein, Murray &
ADDRESSEE: Marchall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
CITY: Ch
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(without alignments)
205.587 Million cell updates/sec
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1 MRRCVRHVLGIGLIVLKNLY.....FQBAFLFFFLILKNPLTLCS
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                           908470 seqs, 133250620 residues
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                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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\$\(\text{SIDS2}/\gagadata/geneseqy-geneseqy-emb1/AA1992.DAT:*\)

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/SIDSZ/gcgdata/geneseqy-geneseqp-embl/AA1986.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:* A_Geneseq_101002:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

70		Description		Secreted protein e	Human nervous syst	Human secreted pro	Human reproductive	Human reproductive	Novel prostate gla	Novel prostate gla	Human polypeptide	Arabidopsis thalia	Arabidopsis thalia
SUMMARIES		£		AAY01442	ABB17898	AAW74772	AAM96017	AAM96695	AAU18865	AAU18919	AA006321	AAG47243	AAG47242
		ä	;	20	22	19	22	22	22	22	22	21	21
		Query Match Length DB		54	82	132	88	89	88	89	66	237	251
	ф	Query	Haccin	100.0	25.8	22.8	22.6	22.6	22.6	22.6	21.2	21.0	21.0
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ALIGNMENTS

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Human; secreted protein; gene therapy; protein therapy; cancer; weight; tumour; chromosome mapping; forensic; haematological disease; allergy; inflammation; cell proliferation; viral infection; wound healing; modulation; appetite; behaviour; food additive; preservative.
                                                                                  Secreted protein encoded by gene 60 clone HOSDK95.
                    AAY01442 standard; Protein; 54 AA.
                                                                                                                                                                                                                                                                                                       970S-0052873.
970S-0052874.
970S-0052875.
970S-0053440.
970S-0053441.
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97US-0052870.
97US-0052871.
97US-0052872.
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                                                             18-MAY-1999 (first entry)
                                                                                                                                                               Homo sapiens
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16-JUL-1997;
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                                          AAY01442;
RESULT 1
          AAY01442
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Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
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2000US-0224518.
2000US-0224519.
2000US-0225213.
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2000US-0227182.
2000US-0227009.
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2000US-0186350
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2000US-0226681
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01-SEP-2000; 2000US-0229344
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                                                                                                                                           WO200159063-A2.
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18-APR-2000;
19-MAY-2000;
07-JUN-2000;
                                                                                                                  Homo sapiens.
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14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
18-AUG-2000;
22-AUG-2000;
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08-SEP-2000;
08-SEP-2000;
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14-AUG-2000;
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01-SEP-2000;
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11-JUL-2000;
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     The invention relates to nucleic acid sequences (AAX22211 to AAX22282)

Concoding human secreted proteins (AAY01383 to AAY01454). The secreted

Corporating gene sequences are deposited with the ATCC under deposit number

ATCC 200138, 209139 or 209141. Host cells containing vectors comprising

the nucleic acid sequences are used for the recombinant expression of

the secreted proteins. The polynucleotide and amino acid sequences are

consequences are used for the recombinant expression of

the secreted proteins. The polynucleotide and amino acid sequences are

useful for preventing, treating or ameliorating medical conditions can

by protein or gene therapy. Pathological conditions can be also diagnosed

by determining the amount of the new polyneptides in a sample or by the

conditions of an useful for chromosome identification

by determining the amount of the new polynucleotides. The nucleic acid

sequences, or its fragments, are useful for chromosome identification

conditions as antissance and triplex-forming therapeutics; in gene

therapy; for (forensic) identification of individuals; as molecular

conditions as antissance and triplex-forming therapeutics; in gene

therapy; for (forensic) identification of individuals; as molecular

conditions as immunoassay reagents (including for in vivo imaging) and

consequences, e.g. autoimmune or haematological diseases,

allergy, inflammation, cancer or other forms of cell proliferation, viral

con other infections. The sequences may also be useful in wound healing,

con other infections. The sequences may also be useful in wound healing,

conditions and as food additive or preservative. The

present sequence represents a human secreted protein (see descriptor

conditions and condition and so food preservative. The

present sequence represents a human secreted protein (see descriptor)
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0
                                                                                                                                                                                                                                                                              New nucleic acids encoding secreted human proteins - potentially useful for treating and diagnosing diseases and identifying specific
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                                                                                                                                                                               Ferrie AM, Florence KA, Fouad J;
Ni J, Rosen CA, Ruben SM, Young PE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human nervous system related polypeptide SEQ ID NO 6555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 283; DB 20;
100.0%; Pred. No. 5.4e-34;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 233; 251pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB17898 standard; Protein; 85 AA
                        970S-0055724.
970S-0055725.
970S-0055726.
970S-0055946.
970S-0055952.
                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
 97US-0053442
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N-PSDB; AAX22270.
                                                                                                                                                                                 Feng P, I
M, Hu J,
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Best Local Similarity
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18-AUG-1997
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immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianemic; antiarthritic; cancer; antiparkinsonian; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiloca, anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine.
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20000S-0246610.
20000S-0246611.
20000S-0246613.
20000S-0249207.
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08-DEC-2000;
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                                                                   27-SEP-2000;
                                                                          29-SEP-2000;
                                                                                        29-SEP-2000;
29-SEP-2000;
                                                                                                                                        02-OCT-2000;
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                                                                                                                                02-OCT-2000;
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                                                                                                                                                                     20-OCT-2000;
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13-OCT-2000
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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are notations e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune chaemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases uch as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                          Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MRRC-----VRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPLTLC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 LRECLLMTCTIRVTAGRGMHILKSLQF------GQIKNPQEQFAVFFLVVKVPILFC 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; testis; tumour; foetal brain tissue; fusion protein; cancer; central nervous system; seizure; diagnosis; neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                      Claim 11; SEQ ID NO 6555; 1701pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 25.8%; Score 73; DB 22; Length 85; Best Local Similarity 30.5%; Pred. No. 0.0068; Matches 18; Conservative 11; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted protein encoded by gene 43 clone HSNBB14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW74772 standard; Protein; 132 AA.
                                                                                                                                                                      Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label= unknown
                                                                                                                                (HUMA-) HUMAN GENOME SCI INC.
                                                    08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
                  2000US-0251869.
2000US-0251989.
  2000US-0251868
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                                                                                                                                                                      Rosen CA, Barash SC,
                                                                                                                                                                                                        WPI; 2001-541565/60.
N-PSDB; ABA14224.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 AA;
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08-DEC-2000;
08-DEC-2000;
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                                      08-DEC-2000;
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9705-0040334
9705-0040336
9705-0040336
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9705-0043313
9705-0043314
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9705-0043569
9705-0043569
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970S-0040161.
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97US-0043669.
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970S-0047586.
970S-0047587.
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97US-0043672.
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97US-0047501.
97US-0047502.
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97US-0047581.
97US-0047582.
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970S-0047598.
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970S-0047600.
970S-0047601.
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97US-0047593.
97US-0047594.
97US-0047595.
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97US-0047615.
97US-0047615.
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970S-0056637.
970S-0056662.
970S-0056664.
970S-0056845.
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97US-0049610
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                             02-OCT-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
11-APR-1997;
                                                                                                                                                                                                                             11 - APR - 1997

11 - APR - 1997

11 - APR - 1997

13 - MAY - 1997

23 - MAY - 1997

24 - MAY - 1997

25 - MG - 1997

25 - MG - 1997

22 - AUG - 1997
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22-AUG-1997
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This sequence represents a secreted human protein encoded by the nucleic acid molecule designated Gene 43 from the human cDNA clone HSNBB14 (deposited as clone ATCC 37945).

The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511-V59812, amino acid sequences AAV74731-W75026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the presence of mutations in the we polynuclectides. Specific uses are described for each of the 186 polynuclectides, based on which tissues they are most highly expressed in (see AAV59511 for described uses).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated human genes and the secreted polypeptide(s) they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;
Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS;
Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;
Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 564-565; 721pp; English.
9705-0056862.
9705-005684.
9705-0056874.
9705-0056875.
9705-0056876.
9705-0056876.
9705-0056876.
9705-0056881.
9705-0056881.
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970S-0056903
970S-0056908
970S-0056910
970S-0056910
970S-0056910
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97US-0057761.
97US-0058785.
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N-PSDB; AAV59553.
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                                                                                                                               22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
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22-AUG-1997
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05-SEP-1997
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Query Match 22.8%; Score 64.5; DB 19; Length 132; Best Local Similarity 37.5%; Pred. No. 0.21; Matches 21; Conservative 9; Mismatches 9; Indels 17; Gaps

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Human; reproductive system related antigen; reproductive system disorder;
                                                                                                     Human reproductive system related antigen SEQ ID NO: 4675.
                        AAM96017 standard; Protein; 89 AA
                                                                                                                                                                                                                                                                                                                                                                      20000S-0205515
20000S-020565
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20000S-022526
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2000US-0227009.
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2000US-0229344.
2000US-0229345.
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2000US-0189874.
2000US-0190076.
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                                                                                                                                                                                                                                                   17-JAN-2001; 2001WO-US01339
                                                                            21-NOV-2001 (first entry)
                                                                                                                                              cancer; gene therapy
                                                                                                                                                                                                WO200155320-A2
                                                                                                                                                                                                                                                                                                                                                                                                             30 - JUN - 2000; 2007 - JUL - 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000
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3-JUN-2000;
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             AAM9601.
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15-SEP-2000; 2
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26-JUL-2000; 2000US-0220964.
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20-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                               Isolated nucleic acid molecule encoding a reproductive system antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                    used in preventing, treating or ameliorating a medical condition
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.6%; Score 64; DB 22; Length 89; 60.0%; Pred. No. 0.15; Live 5; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM96695 standard; Protein; 89 AA.
                                                                                                                                                                                                                                              Rosen CA, Barash SC, Ruben SM,
05-DEC-2000; 2000US-0251030.
05-DEC-2000; 2000US-0251988.
06-DEC-2000; 2000US-025119.
08-DEC-2000; 2000US-0251856.
08-DEC-2000; 2000US-0251868.
08-DEC-2000; 2000US-0251868.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251999.
11-DEC-2000; 2000US-0251990.
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24-FEB-2000; 20000S-0184664.
02-MAR-2000; 20000S-0184564.
16-MAR-2000; 20000S-018974.
17-MAR-2000; 20000S-0190076.
18-APR-2000; 20000S-019123.
19-MAY-2000; 20000S-0205515.
07-JUN-2000; 2000US-0214886.
30-JUN-2000; 2000US-0214886.
                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
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13 LIVLKSFFFFKDSLTPSPRL 32
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Matches 12; Conservative
                                                                                                                                                                                                                                                                             WPI; 2001-465570/50.
N-PSDB; AAL01987.
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Human; nootropic; neuroprotective; cytostatic; antiparkinsonian; antianaemic; dermatological; immunosuppressive; antinflammatory; antiarthritic; antirhemmatic; virucide; hepatotropic; nephrotropic; osteopathic; prostate gland; prostatitis; adenocarcinoma; hair loss; prostatosis; malacoplakia; adenocarcinoma; benign prostatic hypertrophy; hyperplasia; carcinoma; prostate neoplastic disorder; skin aging; reproductive system is prostate neoplastic disorder; skin aging; systemic lupus erythematosus; rheumatoid arthritis; cardiovascular; blood-related disorder; hyperproliferative disorder; respiratory; neurological disorder; hyperproliferative disorder; respiratory;
                                                                                                                                                                                                                                                                                                                                                          liver disorder; wound healing; food preservative.
                                                                                                                                                                                        Novel prostate gland antigen, Seq ID No 164.
                                                                                                        AAU18865 standard; Protein; 89 AA
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20000S-0189874.
20000S-0190076.
20000S-0198123.
20000S-0205515.
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2000US-0215135.
2000US-0216647.
           13 LIVLKNLYFHKNSMYPSPKL 32
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2000US-0224519.
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2000US-0217487.
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2000US-0218290.
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                          2000US-02257
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11.-JUL-2000;
14.-JUL-2000;
26.-JUL-2000;
26.-JUL-2000;
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19-MAY-2000;
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07-JUL-2000;
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18-AUG-2000;
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30-AUG-2000;
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14-AUG-2000;
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24-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acid molecule encoding a reproductive system antigen
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pred. No. 0.15;
5; Mismatches 3; Indels
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2000US-0249244.
2000US-0249245.
2000US-0249264.
2000US-0249265.
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2000US-0249213.
2000US-0249213.
2000US-0249214.
2000US-0249215.
2000US-0249215.
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60.0%;
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2000US-0246611.
2000US-0246613.
2000US-0249207.
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2000US-0249299.
2000US-0249300.
2000US-0250160.
2000US-0250391.
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2000US-0249209.
2000US-0249210.
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2000US-0256719.
2000US-0251479.
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                          2000US-0244617.
                                                     2000US-0246475.
2000US-0246476.
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2000US-0246609.
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Best Local Similarity 60.0
Matches 12; Conservative
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                                        08-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
20-OCT-2000;
20-OCT-2000;
01-NOV-2000;
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05-DEC-2000;
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06-DEC-2000;
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08-DEC-2000;
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17-NOV-2000;
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17-NOV-2000;
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PR 01--SEP-2000; 20000S-022944.
PR 01-SEP-2000; 20000S-022944.
PR 01-SEP-2000; 20000S-022944.
PR 05-SEP-2000; 20000S-022944.
PR 05-SEP-2000; 20000S-022943.
PR 06-SEP-2000; 20000S-022943.
PR 06-SEP-2000; 20000S-0231413.
PR 06-SEP-2000; 20000S-0231414.
PR 08-SEP-2000; 20000S-0231414.
PR 08-SEP-2000; 20000S-0231414.
PR 14-SEP-2000; 20000S-0231414.
PR 14-SEP-2000; 20000S-023329.
PR 25-SEP-2000; 20000S-023339.
PR 25-SEP-2000; 20000S-02346478.
PR 20-CCT-2000; 20000S-0246528.
PR 80-NOY-2000; 20000S-0246528.
PR 80-N
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The invention relates to novel isolated prostate gland related nucleic acids (1) and polypeptides (II). (I) and (II) are useful for diagnosis, proposis, prevention, and/or treatment of diseases and/or disorders of the prostate such as acute non-bacterial prostatitis, chronic non-bacterial prostatitis, prostatitis, prostaticis of prostaticis, granulomatous prostatitis, malacoplakia, benign prostatic prostation, and prostation prostatic disorders, including adenocarcinomas, transitional cell carcinomas, ductal carcinomas, and adenocarcinomas, transitional cell carcinomas, ductal carcinomas, and squamous cell carcinomas, (I), (II) and antibody to (II) are useful for diagnosing and treating reproductive system disorders (Paget's disease), autoimmune disorders (systemic lupus erythematosus, rheumatoid arthritis), blood-related disorders (sickle cell anaemia), hyperproliferative disorders, urinary system disorders (glomerulomephritis), cardiovascular disorders (arrhythmias), cardiovascular disorders (arrhythmias), and neurological disorders (Alzheimer's disorders, musculoskeletal system disorders (and neurological disorders) liver disorders (bliary liver cirrhosis), and neurological disorders (Alzheimer's disorders (conformedial and gall bladder disorders (disorders disorders disor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated prostate gland related polypeptide useful for diagnosis and treatment of disorders of prostate such as prostatodystonia, prostatosis, prostatitis, benign prostatic hypertrophy and malacoplakia
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                                                                                                                                     2000US-0249244.
2000US-0249245.
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2000US-0249265.
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                                         2000US-0249215.
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2000US-0250391.
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N-PSDB; AAS30306.
                                    17-NOV-2000; 2
18-DEC-2000; 2
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RESULT 7

13 LIVLKNLYFHKNSMYPSPKL 32

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Local Similarity 60.0 tes 12; Conservative

Matches

Query Match

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Gaps

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22.6%; Score 64; DB 22; Length 89; 60.0%; Pred. No. 0.15; ive 5; Mismatches 3; Indels

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13-0cT-2000; 20-0cT-2000; 20-0c
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17-NOV-2000;
17-NOV-2000;
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02-0CT-2000;
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02-0CT-2000;
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25-SEP-2000;
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29-SEP-2000;
29-SEP-2000;
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antianaemic; dermatological; immunosupressive; antinflammatory; antianthritic; antirheumatic; virucide; hepatotropic; nephrotropic; csteopathic; prostate gland; prostatitis; adenocarcinoma; halr loss; prostatosis; malacoplakia; adenocarcinoma; benign prostatics hypertrophy; hyperplasia; carcinoma; prostate neoplastic disorder; skin aging; reproductive system disorder; autoimmune disorder; urinary system; systemic lupus erythematosus; rheumatoid arthritis; cardiovascular; blood-related disorder; hyperproliferative disorder; respiratory; neurological disorder; endocrine disorder; inflammatory disorder; liver disorder; wound healing; food preservative.
                                                                                                                                                                                                                                                                                                Human; nootropic; neuroprotective; cytostatic; antiparkinsonian;
                                                                                                                                                                                                                                      Novel prostate gland antigen, Seq ID No 218.
                                     AAU18919 standard; Protein; 89 AA
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14-AUG-2000; 2000US-0225213.
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14-AUG-2000; 2000US-022526.
14-AUG-2000; 2000US-0225470.
14-AUG-2000; 2000US-0225757.
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14-AUG-2000; 2000US-0225759.
18-AUG-2000; 2000US-0225759.
18-AUG-2000; 2000US-0225759.
22-AUG-2000; 2000US-0225759.
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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to sytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hammalopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                        Human, cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inflammation.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; SEQ ID NO 20213; 1399pp + Sequence Listing; English.
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                 Human polypeptide SEQ ID NO 20213.
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated prostate gland related polypeptide useful for diagnosis and treatment of disorders of prostate such as prostatodystonia, prostatosis, prostatitis, benign prostatic hypertrophy and malacoplakia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to novel isolated prostate gland related nucleic
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    05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
11-APR-1999;
21-APR-1999;
23-APR-1999;
23-APR-1999;
30-APR-1999;
30-APR-1999;
30-APR-1999;
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19-MAY-1999;
20-MAY-1999;
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06-MAY-1999;
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07-MAY-1999;
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29-JUN-1999;
30-JUN-1999;
                                                                                                                                                                              11-MAY-1999;
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14-MAY-1999;
                                                                                                                                                                                                                                               21-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 - JUN - 1999;
                                                                                                                                                                                                                                                                                                                                    10-JUN-19
     Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                        Score 59.5; DB 21; Length 237;
Pred. No. 2.3;
8; Mismatches 14; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana protein fragment SEQ ID NO: 59522.
                                                                                                                                                                                                                                                                                                                                                                                  168 GVGCMTAKILRFHQESLNELSQLLQYSSFKFFFFFFYNIV 207
                                                                                                                                                                                                                                                                                                                                                                      10 GIGLIVLKNLYFHKNSMYPSPKL---SSFQEAFLFFFLIL 46
                                                                                                                                                                                                                                                                                                                                                                                                                              AAG47242 standard; Protein; 251 AA.
                                                                                                                                                                                                                                                                                                                                                        8;
99US-0154779.
99US-0155139.
99US-0155486.
                               990S-0156458.
990S-0156596.
990S-0157117.
99US-0157753.
99US-015865.
99US-0158029.
                                                                                                99US-0159293.
99US-0159294.
99US-0159295.
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99US-0159584.
99US-0160741.
99US-0160767.
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99US-0160980.
99US-0160981.
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1 Similarity 37.5%;
15; Conservative 8
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99US-0161360.
99US-0161361.
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99US-0161992.
99US-0161993.
99US-0162142.
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99US-0159637
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99US-0161406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0121825
                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana
                      24 - SEP - 1999;

28 - SEP - 1999;

04 - OCT - 1999;

05 - OCT - 1999;

06 - OCT - 1999;

13 - OCT - 1999;

13 - OCT - 1999;

14 - OCT - 1999;

14 - OCT - 1999;

14 - OCT - 1999;

15 - OCT - 1999;

21 - OCT - 1999;

21 - OCT - 1999;

22 - OCT - 1999;

25 - OCT - 1999;

25 - OCT - 1999;

26 - OCT - 1999;

26 - OCT - 1999;

27 - OCT - 1999;

28 - OCT - 1999;
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Matches
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990S-0143624.
990S-0144005.
990S-0144085.
990S-0144332.
990S-0144331.
990S-0144331.
990S-0144334.
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990S-0149368.
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990S-0155659.
990S-0156458.
990S-0156596.
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19-Jul-1999;
20-Jul-1999;
20-Jul-1999;
20-Jul-1999;
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23-Jul-1999;
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109-AUG-1999)
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23-AUG-1999;
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15-SEP-1999;
16-SEP-1999;
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16-AUG-1999;
17-AUG-1999;
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31-AUG-1999;
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12-AUG-1999;
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22-SEP-1999;
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02-AUG-1999;
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07-SEP-1999;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                                    Length 251;
                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                 Query Match 21.0%; Score 59.5; DB 21; Best Local Similarity 37.5%; Pred. No. 2.4; Matches 15; Conservative 8; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                      10 GIGLIVLKNLYFHKNSMYPSPKL---SSFQEAFLFFFLIL 46
                                                                                                                                                                                                                                                                                                                                                                                                   AAG47241 standard; Protein; 307 AA
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99US-0123180.
99US-0123548.
99US-0126264.
99US-0126285.
99US-01278234.
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990S-0161404-
990S-0161406-
990S-0161406-
990S-0161359-
990S-0161360-
990S-0161992-
990S-0161993-
990S-0161993-
990S-0161993-
990S-0157753.
990S-0158052.
990S-0158022.
990S-0158032.
990S-0159293.
990S-0159293.
990S-0159393.
990S-0159330.
990S-0159330.
990S-0159330.
990S-0159330.
990S-0159638.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana.
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
05-0CT-1999;

06-0CT-1999;

08-0CT-1999;

13-0CT-1999;

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23-0CT-1999;

25-0CT-1999;

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26-0CT-1999;
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20010-0110	90S-01298	9US-01300	9US-01304	9US-01305	90S-01308 90S-01314	9US-01320	9US-01324	9US-01324	90S-01324	9US-01324	9US-01328	9US-01342	9US-01342	9US-01342	9US-01343	9US-01347	9US-01349	9US-01351	9US-01356	3US-01360	30S-01363	9US-013678	9US-013/2	9US-01375(9US-01377	ons-01380	JUS-013854	003-013989 00S-013911	US-01394	OUS-01394	00S-013949	00S-013945	US-01394	US-013945	US-013945	US-013945	US-013946	US-013946	US-013946	10S-013975	US-013981	US-013989	US-014035	US-014069	US-014082	US-014099	US-014184	US-014215	US-014205 US-014239	US-014280	US-014292	US-01429/ US-014354	US-014362	US-014400	US-014408 US-014408	US-014432	99US-0144331.	US-U14433	
01-004-8	6-APR-19	9-APR-19	1-APR-19	3-APR-19	8-APR-19	0-APR-19	0-APR-19	5-MAY-19	6-MAY-19	6-MAY-19	7 - MAY - 199	1 - MAY - 199	4-MAY-19	4-MAY-19	4-MAY-199	8-MAY-199	9-MAY-195	1-MAY-199	1-MAY-199	5-MAY-199	7-MAY-199	3-MAY-195	3-JUN-199	1-JUN-199	-JUN-199	3-JUN-199	- JUN - 199	201-NDC-1	-JUN-199	-JUN-199	-JUN-199	56T-NOC-8	3-JUN-199	-JUN-199	-JUN-199	991-NUC-1	-JUN-199	-JUN-199	-JUN-199	961-NIII-1	-JUN-199	-JUN-199	961-NOC-	-JUN-199	-JUN-199	-JUN-199	-JUL-199	-JUL-199	-JUL-199 -JUL-199	-JUL-199	-JUL-199	-JUL-199	-JUL-199	-JUL-199	-JUL-199 -JUL-199	-JUL-199	19-JUL-1999; 19-JUL-1999;	86T-TOO-	
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90S-01443 90S-01443 90S-01443 90S-01446 90S-01446 90S-01450 90S-01450 90S-01450 90S-01450	990S-0145145. 990S-0145218. 990S-0145218. 990S-0145913. 990S-0145913. 990S-0145919. 990S-0145918. 990S-0145918. 990S-0146388. 990S-0146388. 990S-0147204. 990S-0147204. 990S-0147192. 990S-0147192. 990S-0147193. 990S-0147493. 990S-0147493. 990S-0148319. 990S-0148319. 990S-0148319. 990S-0148319. 990S-0148684. 990S-0148684. 990S-0148684. 990S-0149723. 990S-0149728.	0.00
19-JUL-199 R 19-JUL-199 R 20-JUL-199 R 20-JUL-199 R 20-JUL-199 R 21-JUL-199 R 21-JUL-199 R 22-JUL-199 R 22-JUL-198 R 22-JUL-198 R 22-JUL-199	PR 23 - ULL-1999; PR 23 - ULL-1999; PR 25 - ULL-1999; PR 27 - ULL-1999; PR 27 - ULL-1999; PR 27 - ULL-1999; PR 02 - AUG-1999; PR 02 - AUG-1999; PR 02 - AUG-1999; PR 03 - AUG-1999; PR 05 - AUG-1999; PR 05 - AUG-1999; PR 05 - AUG-1999; PR 10 - AUG-1999; PR 11 - AUG-1999; PR 12 - AUG-1999; PR 11 - AUG-1999; PR 12 - AUG-1999; PR 13 - AUG-1999; PR 20 - AUG-1999; PR 21 - AUG-1999; PR 22 - AUG-1999; PR 23 - AUG-1999; PR 23 - AUG-1999;	23-Aug 1999 25-Aug 1999 27-Aug 1999 27-Aug 1999 30-Aug 1999 30-Aug 1999 31-Aug

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The sequence represents the amino acid sequence of human odorant receptor (OR)-like protein, NOV2. The NOV2 polypeptide, nucleic acid and antibody are useful as therapeutics, particularly in the manufacture of a metibody are useful as therapeutics, particularly in the manufacture of a medicament for treating a syndrome associated with a human disease, which includes a pathology associated with NOV2 polypeptide. The NOV2 nucleic acid and polypeptide are especially useful in therapeutic or prophylactic applications for disorders of the neuro-olfactory system, c. e.g. those induced by trauma, surgery and/or neoplastic disorders. The above conditions. Furthermore, the nucleic acids and polypeptides are useful in treating adenocarcinoma, lymphoma, prostate cancer, uterus cancer, immune response, acquired immunodeficiency synfrome (AIDS), asthma, Crohn's disease, multiple sclerosis or Albright hereditary osteodystrophy. These are also useful in developing powerful assay of system for functional analysis of various human disorders, as well as
                                                          New NOVX polypeptides and polynucleotides, useful for treating or preventing disorders of the neuro-olfactory system, cancer and multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists \dot{}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yanai I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RRCVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPL---TLCS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.8%; Score 59; DB 22; Length 310; 30.4%; Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fuchs T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human olfactory receptor polypeptide, SEQ ID NO: 1122.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lancet D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG71441 standard; Protein; 310 AA
                                                                                                                                   Claim 1; Page 16; 141pp; English.
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(YEDA ) YEDA RES & DEV CO LTD.
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24-FEB-2000; 2000US-0184809.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     in diagnostic applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 20.8'
Best Local Similarity 30.4'
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-290713/30.
            WPI; 2001-451859/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 310 AA;
                           N-PSDB; AAS09946
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                                                                                                  sclerosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.0%; Score 59.5; DB 21; 37.5%; Pred. No. 3.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 GIGLIVLKNLYFHKNSMYPSPKL --- SSFQEAFLFFFLIL 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human odorant receptor (OR)-like protein, NOV2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU05132 standard; Protein; 310 AA
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2000US-0178191.
2000US-0178227.
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99US-0160815.
99US-0160980.
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99US-0161404.
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99US-0161359.
99US-0161360.
99US-0161920.
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99US-0161993.
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2000US-0220253.
2000US-0220590.
                                                                 99US-0159637.
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99US-0159584.
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                                                                                                                    99US-0160741.
99US-0160767.
                                                                                                                                                         99US-0160768.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Li L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200151632-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JAN-2000;
26-JAN-2000;
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24-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L4 - JAN - 2000;
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                                                                                                                                                                                          L-OCT-1999;
L-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUL-2001.
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Spytek KA,
                                                                                                                                                       21-0CT-1999;
21-0CT-1999;
                                                                                                                                                                                                                                                                                                  666
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29-OCT-1999;
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                                                      -OCT-1999
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25-0CT-1
                                                                   14-0CT-1
14-0CT-1
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                                                                                                                                        31-OCT-
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re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory

faculties of different individuals.

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                                                     The present sequence is an olfactory receptor which is encoded by one of a number of novel polynucleotides. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods of the odour receptors used to detect these primary scents. The methods combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different individuals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           involved in olfactory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yanai I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54
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9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRCVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPL---TLCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides which encode polypeptides involved in olf sensation for identifying olfactory agonists and antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 59; DB 22; Length 310;
Pred. No. 3.7;
9; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fuchs T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human olfactory receptor polypeptide, SEQ ID NO: 1153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glusman G,
Claim 11; Page 646-647; 1857pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG71472 standard; Protein; 310 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lancet D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DIGI-) DIGISCENTS.
(YEDA ) YEDA RES & DEV CO LTD.
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24-FEB-2000; 2000US-0184809.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-OCT-2000; 2000WO-US27582.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 30.45
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-290713/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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ò g The present sequence is an olfactory receptor which is encoded by one of a number of novel polynucleotides. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods sto enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to

Claim 11; Page 672-673; 1857pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 designated PHOR1-All and PHOR1-F5D6 and their encoded proteins. The gene encoding PHOR1-All and PHOR1-F5D6 and their encoded proteins. The PHOR1-F5D6 maps to chromosome 1q23, and the gene encoding PHOR1-F5D6 maps to chromosome 7q33-q35. The PHOR1-All and PHOR1-F5D6 polyhoucheotide and polypeptide sequences are useful in diagnostic and therapeutic methods, and compositions for various cancers such as prostate cancer. The sequences are useful for inhibiting the growth of cancer calls that express PHOR1-All or PHOR1-F5D6 and for treating cancer. The PHOR1-All or PHOR1-F5D6 polypeptide or a fragment thereof can be used to elicit an immune response. The present sequence represents human PHOR1-F5D6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of cancer in subject, by determining status of PHOR1-A11/PHOR1-F5D6 gene products in tissue sample from subject and comparing it to normal sample
                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                      238 RICFSHLCVIGLVYGTAIIMYVGPRYGNPK---EOKKYLLLFHSLFNPMLNPLICS 290
                                                                                                                                                                2 RRCVRHVLGIGLIVLKNLYFHKNSMYPSPKLSSFQEAFLFFFLILKNPL---TLCS 54
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9
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                                                                                                          DB 22; Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.8%; Score 59; DB 23; Length 310; 30.4%; Pred. No. 3.7;
                                                                                                                    3.7;
Thes 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                Human; PHOR1-A11; PHOR1-F5D6; prostate cancer; cytostatic.
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                                                                                                                                     9; Mismatches
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                                                                                                        Score 59;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                    Human PHOR1-F5D6 amino acid sequence.
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                                                                                                                        Pred.
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                                                                                                        20.8%;
                                                                                                                       30.4%;
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                                                                                                Query Match
Best Local Similarity 30.49
Matches 17; Conservative
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                                                                          310 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                            Sequence
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Db 238 RTCFSHLCVIGLVYGTAIIMYVGPRYGNPK---EQKKYLLLFHSLFNPMLNPLICS 290

Search completed: November 21, 2002, 13:41:32 Job time : 37 secs

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